

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 26, 2002, 06:09:02 : Search time 24.01 Seconds
(without alignments)
667.127 Million cell updates/sec

Title: US-09-701-121-2
Perfect score: 649
Sequence: 1 PLATGKRPKSNLKARSR.....ANNVYKQVDMVVESSGR 119

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Scatched: 522463 seqs, 74073290 residues
Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_1101.*
1: /SIUS8/qcdata/qeneseq/qeneseq/AA1980.DAT.*
2: /SIUS8/qcdata/qeneseq/qeneseq/AA1981.DAT.*
3: /SIUS8/qcdata/qeneseq/qeneseq/AA1982.DAT.*
4: /SIUS8/qcdata/qeneseq/qeneseq/AA1983.DAT.*
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8: /SIUS8/qcdata/qeneseq/qeneseq/AA1987.DAT.*
9: /SIUS8/qcdata/qeneseq/qeneseq/AA1988.DAT.*
10: /SIUS8/qcdata/qeneseq/qeneseq/AA1989.DAT.*
11: /SIUS8/qcdata/qeneseq/qeneseq/AA1990.DAT.*
12: /SIUS8/qcdata/qeneseq/qeneseq/AA1991.DAT.*
13: /SIUS8/qcdata/qeneseq/qeneseq/AA1992.DAT.*
14: /SIUS8/qcdata/qeneseq/qeneseq/AA1993.DAT.*
15: /SIUS8/qcdata/qeneseq/qeneseq/AA1994.DAT.*
16: /SIUS8/qcdata/qeneseq/qeneseq/AA1995.DAT.*
17: /SIUS8/qcdata/qeneseq/qeneseq/AA1996.DAT.*
18: /SIUS8/qcdata/qeneseq/qeneseq/AA1997.DAT.*
19: /SIUS8/qcdata/qeneseq/qeneseq/AA1998.DAT.*
20: /SIUS8/qcdata/qeneseq/qeneseq/AA1999.DAT.*
21: /SIUS8/qcdata/qeneseq/qeneseq/AA2000.DAT.*
22: /SIUS8/qcdata/qeneseq/qeneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	649	100.0	119	21	AAV44296
2	645	99.4	119	17	AAW06920
3	645	99.4	119	18	AAW19846
4	645	99.4	120	16	AAW78731
5	645	99.4	120	18	AAW26590
6	645	99.4	120	14	AAW40800
7	645	99.4	501	16	AAW69600
8	645	99.4	501	12	AAW36100
9	645	99.4	501	18	AAW19210
10	645	99.4	501	18	AAW11900
11	645	99.4	501	18	AAW01799

12	645	99.4	501	18	AAW12770	Human bone morphol
13	645	99.4	501	19	AAW44868	TGF-beta super fami
14	645	99.4	501	19	AAW44008	Human MP52, Homo
15	645	99.4	501	22	AAW70529	Human TGF-beta MP5
16	640	98.6	495	15	AAW60022	Growth diff. regulat
17	640	98.6	495	22	AAW44550	Amino acid sequenc
18	639	98.5	119	21	AAW70752	Wild type mature b
19	639	98.5	119	21	AAW70756	Methionine oxidase
20	639	98.5	119	21	AAW70757	Methionine alkylat
21	639	98.5	119	21	AAW70758	Tryptophan alkylsu
22	639	98.5	501	17	AAW95635	Cartilage-derived
23	639	98.5	501	21	AAW92034	Human growth diff
24	559	86.1	102	21	AAW09554	Human BMP-1/GDF-5
25	559	86.1	102	21	AAW02819	Human BMP-1/GDF-5
26	559	86.1	102	21	AAW92578	BMP-1/GDF-5 finge
27	543	83.7	134	16	AAW66867	GDF-6, Mus sp. A
28	543	83.7	134	21	AAW12986	Murine growth diff
29	543	83.7	263	16	AAW78739	Murine m22 protein
30	543	83.7	263	18	AAW26595	Murine BMP-13 homo
31	540	83.2	421	16	AAW78730	Human mature VEGF
32	540	83.2	421	18	AAW26591	Human bone morphol
33	528	81.4	436	17	AAW95636	Cartilage derived
34	510	78.6	102	21	AAW09555	Murine GDF-6, SHG
35	510	78.6	102	21	AAW02821	Mouse GDF-6, amino
36	510	78.6	102	21	AAW92580	GDF-6 finge-1 like
37	507	78.1	102	21	AAW09554	Human BMP-2/GDF-6
38	507	78.1	102	21	AAW02820	Human BMP-2/GDF-6
39	507	78.1	102	21	AAW92579	BMP-2/GDF-6 finge
40	495	76.3	102	21	AAW09556	Bovine BMP-2, SE
41	495	76.3	102	21	AAW02822	Bovine BMP-2, amin
42	495	76.3	102	21	AAW92581	BMP-2 finge-1 like
43	494	76.1	129	19	AAW54067	Bone morphogenetic
44	494	76.1	294	16	AAW78729	Human bone morphol
45	494	76.1	294	18	AAW01589	Human bone morphol

ALIGNMENTS

RESULT 1	
AAV44296	
ID	AAV44296 standard; Protein: 119 AA.
XX	
AC	AAV44296:
XX	
XX	29-FEB-2000 (first entry)
DE	Mutant human MP52 monomer protein.
XX	
XX	Mutant MP52 monomer protein; transforming growth factor-beta; TGF-beta;
KW	pKOT279 expression vector; osteocyte; bone morphogenetic; osteopathic;
KW	anti-arthritic activity; cartilage; osteoporosis; osteoarthritis;
KW	arthroosteoitis; fracture; achondroplasia; dyschondrogenesis;
KW	achondrogenesis; palatoschisis; dysosteoconosis.
XX	
XX	Homo sapiens.
XX	Synthetic.
XX	
XX	Key Location/Qualifiers
FT	Misc-difference 83
FT	/note "Wild-type Cys replaced by Ala"
XX	
XX	W09961611-AL.
XX	
XX	02-DEC-1999.
XX	
XX	14-MAY-1999: 99W0-1100866.
XX	
XX	22-MAY-1998: 98JP-0141379.
XX	
XX	(HMR1) H007HS1 MARFON ROUSSEL LTD.
XX	
XX	Kawai S., Kimura M., Muraki Y., Katsunra M.

XX WP1: 2000-097122/08.
 DR N-PSDB: AAZ29428.
 XX Novel monomer protein used for prevention and treatment of bone and/or
 PT cartilage diseases
 XX Claim 4; Page 20; 26pp; English.
 PS The present sequence is a mutant human MP52 monomer protein, which
 CC belongs to transforming growth factor-beta (TGF beta)
 CC superfamily. Mutant MP52 can be produced in E. coli cells by
 CC transforming them with pKOT279 expression vector containing a mutated
 CC MP52 monomer encoding nucleic acid sequence. MP52 monomer protein is
 CC capable of inducing differentiation in osteocytes and exhibits bone
 CC morphogenetic, osteopathic and anti-arthritis activity. The MP52 monomer
 CC protein is used for prevention and treatment of cartilage and/or bone
 CC diseases such as osteoporosis, osteoarthritis, arthritis, damage of
 CC cartilage, regeneration of bone, cartilage defect caused by injury and
 CC tumour dissection, fracture, congenital bone and/or cartilage diseases
 CC such as achondroplasia, dyschondrogenesis, achondrogenesis, palatoschisis
 CC and dysostegenesis and a deficit of root of teeth and a tooth socket.
 XX Sequence 119 AA;
 SQ

Query Match 100.0%; Score 649; DB 21; Length 119;
 Best Local Similarity 100.0%; Pred. No. 40-60;
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PLATRCRKPSKNIKAGCSKKALHVNFKMGWDWLIAPLEYAFHVEFVPSHLE 60
 DB 1 platrqrkpskni karcskalkhvnfkmdwdwliapleyafhveefvpslshle 60
 QY 61 PTNHAVIQLTMSMDPESTPTTACVPTPLSPISLIFDSANNVVKYEDMVVESVGR 119
 DB 61 ptuhaviqltmsmdpestpttaccvptplspisllfidsannvvkyedmvvesvgr 119
 DB 61 ptuhaviqltmsmdpestpttaccvptplspisllfidsannvvkyedmvvesvgr 119

RESULT 2
 AAW06920
 ID AAW06920 standard; Protein; 119 AA.
 XX AAW06920;
 AC
 XX 27-JUN 1997 (first entry)
 PT Human MP52 growth factor residues 484-501.
 DE
 XX Human; MP52; growth factor; monomer; dimer; treatment; bone;
 KW cartilage; dental; disorder; fracture; bone loss;
 KW periodontal disease; calcification; osteoporosis.
 XX
 OS Homo sapiens.
 XX
 XX W09633215-A1.
 FN 24-OCT 1996.
 XX
 XX 19 APR 1996; 96BO JP01062.
 XX
 XX 17-NOV 1995; 95JP 0322404.
 PR 19-APR 1995; 95JP-0094664.
 XX
 XX (FARH) BIOQUEST JAPAN LTD.
 PA
 XX Enomoto K., Katsura M., Kawai S., Kimura M., Makishima H;
 P1 Matsumoto T., Miki H., Satoh Y., Takamatsu H;
 XX
 XX WP1: 1996-485740/48.
 DR N-PSDB: AA146150.
 XX Peptide consisting of part of human MP52 growth factor, and its

PT dimer is used for treatment of bone, cartilage and dental
 PI disorders
 XX Claim 1; Pages 16-19; 4pp; Japanese.
 PS The present sequence is residues 484 to 501 of the human MP52
 CC growth factor, a dimer of which can be used to treat bone,
 CC cartilage and dental disorders, including fractures, bone loss and
 CC periodontal disease. The dimer was prepared by transforming a host
 CC (preferably E. coli) with a suitable (plasmid) expression vector
 CC containing DNA encoding the monomer. The host was cultured, and
 CC inclusion bodies from the cells worked up to give the monomer,
 CC which was then converted into the dimer. The product was mixed with
 CC type 1 pig tendon collagen and injected into the large thigh vein
 CC of 1CR mice. After 20 days 4 of 4 mice injected with 10 microg of
 CC the dimer showed bone/cartilage calcification around the injection
 CC site, compared to none in 0 of 4 mice treated with collagen only.
 XX Sequence 119 AA;
 SQ

Query Match 99.4%; Score 645; DB 17; Length 119;
 Best Local Similarity 99.2%; Pred. No. 10-59;
 Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLATRCRKPSKNIKAGCSKKALHVNFKMGWDWLIAPLEYAFHVEFVPSHLE 60
 DB 1 platrqrkpskni karcskalkhvnfkmdwdwliapleyafhveefvpslshle 60
 QY 61 PTNHAVIQLTMSMDPESTPTTACVPTPLSPISLIFDSANNVVKYEDMVVESVGR 119
 DB 61 ptuhaviqltmsmdpestpttaccvptplspisllfidsannvvkyedmvvesvgr 119
 DB 61 ptuhaviqltmsmdpestpttaccvptplspisllfidsannvvkyedmvvesvgr 119

RESULT 3
 AAW19846
 ID AAW19846 standard; Protein; 119 AA.
 XX AAW19846;
 AC
 XX 12-FEB 1998 (first entry)
 PT Human bone inducing factor MP52.
 DE
 XX Human; bone inducing factor; MP52; collagen; fracture;
 KW polyoxyethylene polyoxypropylene glycol.
 KW
 XX Homo sapiens.
 OS
 XX W09718829-A1.
 FN 29-MAY 1997.
 XX
 XX 14-NOV-1996; 96WO JP033333.
 XX
 XX 17-NOV-1995; 95JP 0322402.
 PR (FARH) BIOQUEST JAPAN LTD.
 PA (FARH) BIOQUEST PHARM & CHEM KK.
 XX
 XX Shimura T., Toyama S;
 PT
 XX WP1: 1997-410249/28.
 DR N-PSDB: AA170296.
 XX Material for repairing bone and collagen, especially bone fracture
 PT or loss, comprising bone inducing factor and
 PT polyoxyethylene polyoxypropylene glycol compounds
 XX
 XX Example 4; Page 16-17; 4pp; Japanese.
 XX Bone and collagen inducing material has been developed which comprises
 CC bone inducing factor and polyoxyethylene polyoxypropylene glycol


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Query Match          99.4%; Score 645; DB 18; Length 120;
Best Local Similarity 99.2%; Pred. No. 1; 59;
Matches 116; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLATROCKRPSKNIKARC SRKALIVNFKDMCWDOWI LAPIEYAFR EBI CEFPLKSHLE 60
DB 1 PLATROCKRPSKNIKARC SRKALIVNFKDMCWDOWI LAPIEYAFR EBI CEFPLKSHLE 60
DB 2 PLATROCKRPSKNIKARC SRKALIVNFKDMCWDOWI LAPIEYAFR EBI CEFPLKSHLE 60
QY 61 PINHAVIQTILMNSMDPESTPTACVPTRELSPLSLFIDISANNVVYKQYELMVVESGCR 119
DB 62 PINHAVIQTILMNSMDPESTPTACVPTRELSPLSLFIDISANNVVYKQYELMVVESGCR 120

RESULT 6
AAK40800
ID AAK40800 standard; Protein; 401 AA.
XX
XX AAK40800;
XX
XX 11-FEB-1994 (first entry)
XX
XX TGF-beta-like clone MP-52 protein.
XX
XX Human; transforming growth factor; beta; TGF-beta; pharmacological;
XX bone; cartilage; tooth; wound repair; immunosuppressor;
XX organ transplant; cosmetic surgery; antibody; diagnostics.
XX
XX Homo sapiens.
XX
XX W09416099 A.
XX
XX 19 AUG-1993.
XX
XX 12 FEB-1993; 9360-EP00450.
XX
XX 12-FEB-1992; 92EP-0102424.
XX
XX (BLOP-) BIOPHARM GES BIOTECHNOLAGISCHEN ENTWICKL.
XX
XX Boettgen G., Neidhardt H.
XX
XX WP1: 1994-272824/44.
XX
XX N PSDB: AAQ47769.
XX
XX New transforming growth factor-beta family proteins and DNA
XX used in tissue and wound repair, in treatment of bone, cartilage
XX and tooth defects, and antibodies for diagnosis
XX
XX Claim 11; Page 19; 29pp; English.
XX
XX The sequences given in AAK40800 and AAK45447 represent fragments of
XX embryo and liver derived human transforming growth factor beta
XX (TGF-beta) respectively. The full length protein may be used in a
XX pharmaceutical composition for the treatment of various bone, cartilage
XX or tooth defects and in tissue and wound repair processes. These
XX proteins may also be used as immunosuppressors in organ transplants and
XX in cosmetic surgery. Antibodies raised against these proteins may be
XX used for diagnostic purposes.
XX
XX Sequence 401 AA;

Query Match          99.4%; Score 645; DB 14; Length 401;
Best Local Similarity 99.2%; Pred. No. 4; 59;
Matches 116; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLATROCKRPSKNIKARC SRKALIVNFKDMCWDOWI LAPIEYAFR EBI CEFPLKSHLE 60
DB 283 PLATROCKRPSKNIKARC SRKALIVNFKDMCWDOWI LAPIEYAFR EBI CEFPLKSHLE 442
QY 61 PINHAVIQTILMNSMDPESTPTACVPTRELSPLSLFIDISANNVVYKQYELMVVESGCR 119
DB 62 PINHAVIQTILMNSMDPESTPTACVPTRELSPLSLFIDISANNVVYKQYELMVVESGCR 120
DB 63 PINHAVIQTILMNSMDPESTPTACVPTRELSPLSLFIDISANNVVYKQYELMVVESGCR 401

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RESULT 7
AAK69600
ID AAK69600 standard; Protein; 501 AA.
XX
XX AAK69600;
XX
XX 10 OCT-1995 (first entry)
XX
XX New TGF-beta family member MP-52 protein sequence.
XX
XX Transforming growth factor beta family; mitogenic; differentiation;
XX treatment; prevention; disease; bone; cartilage; connective tissue;
XX skin; mucosa; epithelium; dental tissue; wound healing; osteoporosis;
XX tissue regeneration; arthritis; SS.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 482
XX /Label mature protein
XX
XX W09504819 A.
XX
XX 16 FEB-1995.
XX
XX 09 AUG-1994; 94WO 8102640.
XX
XX 10 AUG-1995; 94DE 4326829.
XX
XX 25 MAY-1994; 94DE 4418222.
XX
XX 09 JUN-1994; 94DE 4420157.
XX
XX (BLOP-) BIOPHARM GES BIOTECHNOLAGISCHEN ENTWICKL.
XX
XX Boettgen G., Neidhardt H., Paulista M., Boettgen G.
XX
XX WP1: 1995-090897/12.
XX
XX N PSDB: AAQ64695.
XX
XX New DNA encoding a new member of the TGF-beta family and
XX related vectors, host cells etc., has mitogenic and
XX differentiation inducing activity, e.g., for treating or
XX preventing diseases of bone and cartilage etc.
XX
XX Claim 6; Page 46; 51pp; German.
XX
XX The amino acid sequence of a novel member of the transforming growth
XX factor beta (TGF-beta) family named MP-52. The gene encodes a protein
XX of 501 amino acids (AA). The protein, or at least the mature protein,
XX has mitogenic and/or differentiation inducing properties useful in
XX the treatment or prevention of diseases of bone, cartilage, connective
XX tissue, skin, mucosa, epithelium or dental tissue. The protein can also
XX be used for wound healing and tissue regeneration e.g. in osteoporosis
XX and arthritis.
XX
XX Sequence 501 AA;

Query Match          99.4%; Score 645; DB 16; Length 501;
Best Local Similarity 99.2%; Pred. No. 5; 59;
Matches 116; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLATROCKRPSKNIKARC SRKALIVNFKDMCWDOWI LAPIEYAFR EBI CEFPLKSHLE 60
DB 483 PLATROCKRPSKNIKARC SRKALIVNFKDMCWDOWI LAPIEYAFR EBI CEFPLKSHLE 442
QY 61 PINHAVIQTILMNSMDPESTPTACVPTRELSPLSLFIDISANNVVYKQYELMVVESGCR 119
DB 62 PINHAVIQTILMNSMDPESTPTACVPTRELSPLSLFIDISANNVVYKQYELMVVESGCR 120
DB 63 PINHAVIQTILMNSMDPESTPTACVPTRELSPLSLFIDISANNVVYKQYELMVVESGCR 501

```

RESULT 8

AAW46100
ID AAW46100 standard; Protein: 501 AA.

XX
AC AAW46100;

XX
DT 08-MAY-1998 (first entry)

XX
DE Human MP52.

XX
KW Bone morphogenetic protein; BMP: processing enzyme; MP52;
KW BMP-2; BMP-4; BMP-6; BMP-7; bone formation; bone regeneration.

XX
OS Homo sapiens.

XX
PN W09741250-A1.

XX
PD 06-NOV-1997.

XX
PF 28-APR-1997; 97W01JP01474.

XX
PR 30-APR-1996; 96JP-0140618.

XX
PA (FAHH) HOECHST YAKUHIN KOGYO KK.

XX
PA (FAHH) HOECHST PHARM & CHEM KK.

XX
PI Kimura M, Makishima F, Takahashi M;

XX
DR WPI: 1997-544748/50.

XX
DR N-PSDB; AAT98191.

XX
PT Production of mature bone morphogenetic protein - by treatment of
PT precursor protein with a processing enzyme such as furin either
PT directly or by expressing them both in the same host

XX
PS Example 1; Pages 21-25; 4pp; Japanese.

XX
CC The present sequence is MP52, which is a bone morphogenetic
CC protein (BMP).

CC
CC Mature BMP can be produced by directly adding a BMP processing
CC enzyme to a solution containing BMP precursor protein, or by

CC
CC transforming an animal cell with expression vectors containing DNA
CC encoding the enzyme and precursor protein, culturing the

CC
CC transformant and isolating the mature BMP from the culture. The
CC method can be used to produce MP52, BMP-2, BMP-4, BMP-6 and BMP-7,

CC
CC which can be used to treat bone formation or regeneration
CC abnormalities.

XX
SQ Sequence 501 AA:

Query Match 99.4%; Score 645; DB 18; Length 501;

Best Local Similarity 99.2%; Pred. No. 5, 90-59;

Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLATRGCKRPSKNIKARCSKALHVNFKOMGWDWIIAPLEYEAFHCHGEGEPLRSHLE 60

DB 384 platrqkrrpsknlkarcsrkahvntkdmqddwiiapleyeathceqlceiprshle 442

QY 61 PTNHAVIQTLMNSMDPESTPTTACVPTRLSPISILFIDSANNVYKQYEMVVSQGR 119

DB 443 plnhavtqlmnsmdpepttpttcevtprlspisilfidsannvvykqyedmvvscegr 501

RESULT 9

AAW19210

ID AAW19210 standard; Protein: 501 AA.

XX
AC AAW19210;

XX
DT 04-MAR-1998 (first entry)

XX
DE Human TGF-beta protein MP52.

XX

KW

KW Human transforming growth factor-beta; TGF-beta; MP52; superfamily;

XX
XX cartilage; bone inducing activity; inhibit; bone resorption.

OS Homo sapiens.

XX
PN DE19548476-A1.

XX
PD 26-JUN-1997.

XX
PF 22-DEC-1995; 95DE-1048476.

XX
PR 22-DEC-1995; 95DE-1048476.

XX
PA (BIOF-) BIOFARM GES BIOTECHNOLOGISCHEN ENTWICKL.

XX
PI Hechtold K, Botton G, Paulista M, Pohl J, Hechten G;

XX
DR WPI: 1997-33931/41.

XX
DR N-PSDB; AA169045.

XX
PT Compound containing protein from TGF-beta superfamily has bone
PT and/or cartilage inducing activity, useful in treatment of, e.g.,
PT osteoporosis, bone damage, Paget's disease and osteoarthritis

XX
PS Claim 3; Page 9; 10pp; German.

XX
CC This sequence is the human transforming growth factor (TGF)-beta protein
CC designated MP52. MP52 can be used in a compound of formula (I):
CC A-X(1-20) B(1-20) (I); A = protein, or fragment, of the TGF-beta
CC superfamily with cartilage and/or bone inducing activity (e.g. MP52);
CC B = 1 or more substituent groups with an affinity to the extracellular
CC matrix, cellular components of bone and/or cartilage and/or to a
CC biocompatible carrier matrix; X = 1 or more covalent bonds and/or spacer
CC groups. The compound may be used to inhibit bone resorption, prevent or
CC treat bone or cartilage related disorders, including osteoporosis,
CC Paget's disease, osteodystrophy, osteoarthritis or osteoarthritis and
CC to treat bone or cartilage damage caused by wounding or overloading.

XX
SQ Sequence 501 AA:

Query Match 99.4%; Score 645; DB 18; Length 501;

Best Local Similarity 99.2%; Pred. No. 5, 90-59;

Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLATRGCKRPSKNIKARCSKALHVNFKOMGWDWIIAPLEYEAFHCHGEGEPLRSHLE 60

DB 384 platrqkrrpsknlkarcsrkahvntkdmqddwiiapleyeathceqlceiprshle 442

QY 61 PTNHAVIQTLMNSMDPESTPTTACVPTRLSPISILFIDSANNVYKQYEMVVSQGR 119

DB 443 plnhavtqlmnsmdpepttpttcevtprlspisilfidsannvvykqyedmvvscegr 501

RESULT 10

AAW11900

ID AAW11900 standard; Protein: 501 AA.

XX
AC AAW11900;

XX
DT 28-OCT-1997 (first entry)

XX
DE Human high mol. wt. protein MP52, a growth/differentiation factor.

XX
KW Growth factor; differentiation; bone induction; osteoporosis; teeth;
KW tooth; dental; joint tissue; cartilage; mucous membrane; skin; nails;
KW wound healing; regeneration; skeletal disorder; fracture; dimer.

XX
OS Homo sapiens.

XX
PN W09704095-A1.

XX
PD 06-FEB-1997.

DR N-PSUB: AAT59729.
 XX
 CC New human bone morphogenic factor, MP52 Arg - used in the treatment
 PT of osteoporosis and bone fracture, and for promoting bone regrowth
 XX
 CC Claim 1: Page 12-15; 26pp; English.
 PS
 XX
 CC Novel human bone morphogenic factor MP52 Arg (AAW12770) is a growth
 CC factor that induces formation of cartilage from undifferentiated
 CC mesenchymal cells and which stimulates the differentiation and
 CC maturation of osteoblasts. It is effective for treating/preventing
 CC bone diseases caused by abnormal bone metabolism such as
 CC osteoporosis. It also accelerates the healing of bone fractures,
 CC and is useful for orthopaedic reconstruction, bone transplantation,
 CC and dental therapeutics because of its bone morphogenetic activity.
 CC It is also effective for preventing/treating cartilage, skin,
 CC connective tissue, mucous membrane, teeth and epithelial disorders.
 CC Recombinant MP52 Arg can be produced in host (e.g. CHO) cells
 CC utilising an isolated DNA sequence (AAT59729) in plasmid pMSS99.
 XX
 CC Sequence 501 AA;
 SQ

Query Match 99.4%; Score 645; DB 19; Length 501;
 Best Local Similarity 99.2%; Pred. No. 5,9e-59;
 Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLATROGRPSKSLKARCSRKALHVNPKMGMDWI IAPLEYAFHCEGLCEPPLRSKLE 60
 DB 383 PLATQGRPSKSLKARCSRKALHVNKMGMDWI IAPLEYAFHCEGLCEPPLRSKLE 60
 QY 61 PTNHAVIQTLNMSMDPESTPTACVPTSPISIFIDSNANNVVKYFIMVVESGGR 119
 DB 443 PTNHAVIQTLNMSMDPESTPTACVPTSPISIFIDSNANNVVKYFIMVVESGGR 501

RESULT 13
 AAW44868
 ID AAW44868 standard; protein: 501 AA.
 AC AAW44868;
 XX
 XX 24-SEP-1998 (first entry)
 DE IGF-beta superfamily subunit.
 XX
 XX IGF-beta; calcium phosphate matrix; bioactive implant; parodontosis;
 KW bone replacement; cartilage; bone; fracture.
 XX
 XX Synthetic.
 XX DE19647854-A1.
 XX
 XX 20-MAY-1998.
 XX
 XX 19-NOV-1996; 96DE-1047853.
 XX
 XX 19-NOV-1996; 96DE-1047853.
 XX
 XX (HIOF-) GICHARM GES BIOTECHNOLOGISCHEN ENTWICKL.
 PA (GERO-) GERONTOCARE GMBH BIOMATERIALS & MEDICAL.
 XX
 XX Heide H, Pabst J, Paulista M, Pohl J;
 XX WPI: 1998-087890/26.
 XX
 XX Bioactive implant material for bone replacement - comprising
 PT osteogenic calcium phosphate matrix coated with protein
 PS
 XX Claim 3: Page 8-10; 12pp; German.
 XX
 CC The IGF-beta superfamily subunit can be used together with a calcium
 CC phosphate matrix to produce a bioactive implant material for bone

CC replacement. The implant has cartilage anabolic bone-forming activity and
 CC can be used for local treatment of cartilage and/or bone diseases or
 CC damage caused by trauma, surgery, denervation or overloading. The
 CC implant can also be used for the treatment of bone defects, e.g.
 CC parodontosis or fractures and in cosmetic and plastic surgery for fixing
 CC mobile bones.
 XX
 CC Sequence 501 AA;
 SQ

Query Match 99.4%; Score 645; DB 19; Length 501;
 Best Local Similarity 99.2%; Pred. No. 5,9e-59;
 Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLATROGRPSKSLKARCSRKALHVNPKMGMDWI IAPLEYAFHCEGLCEPPLRSKLE 60
 DB 383 PLATQGRPSKSLKARCSRKALHVNKMGMDWI IAPLEYAFHCEGLCEPPLRSKLE 60
 QY 61 PTNHAVIQTLNMSMDPESTPTACVPTSPISIFIDSNANNVVKYFIMVVESGGR 119
 DB 443 PTNHAVIQTLNMSMDPESTPTACVPTSPISIFIDSNANNVVKYFIMVVESGGR 501

RESULT 14
 AAW44008
 ID AAW44008 standard; protein: 501 AA.
 XX
 AC AAW44008;
 XX
 XX 22-MAY-1998 (first entry)
 DE Human MP52.
 XX
 XX Human MP52; mouse monoclonal antibody; Mab; purification;
 KW assaying.
 XX
 XX Homo sapiens.
 XX
 XX Key: Location/Qualifiers
 FT Peptide 1..27
 FT /label seq_peptide
 FT 28..501
 FT /label mat_peptide
 XX
 XX W69743408 A1.
 XX
 XX 20-NOV-1997.
 XX
 XX 13-MAY-1997; 97W6-JH01603.
 XX
 XX 07-MAY-1997; 97JP-0131631.
 XX
 XX 13-MAY-1996; 96JP-0141137.
 XX
 XX (FARB) BIOHIST PHARM & CHEM KK.
 XX
 XX Jitsukawa I, Kitadawa H, Nakadawa H, Yanadisawa S;
 XX WPI: 1998-08877/01.
 XX N-PSUB: AAT58340.
 XX
 XX Mouse anti-human MP52 monoclonal antibody - recognises the dimeric
 PT form of MP52 but not the monomer, and does not cross-react with
 PT IGF-beta or BMP-2
 XX
 XX Disclousure: Pages 31-35; 46pp; Japanese.
 XX
 XX The present sequence, human MP52, was used in the
 CC preparation of a novel mouse monoclonal antibody (Mab), which
 CC recognises dimeric but not monomeric human MP52. The Mab has a
 CC heavy chain of subclass gamma, and does not cross-react with
 CC IGF-beta or BMP-2. The Mab may be used to purify and assay human
 CC MP52, especially recombinant MP52.
 XX

cc dental implants, neural tissue including CNS tissue and neuroepithelial
cc situations, tissue of the sensory system, liver, pancreas, cardiac,
cc blood vessels, renal, uterine and thyroid tissue, skin, mucous membrane,
cc endothelium, epithelium, for promotion or induction of nerve growth,
cc tissue regeneration, and/or for treatment of wound healing including ulcers, burns,
cc injuries of skin grafts, induction of proliferation of progenitor cells
cc or bone marrow cells, for maintenance of a state of proliferation or
cc differentiation, for treatment or preservation of tissue or cells for
cc organ or tissue transplantation, for integrity of osteointegration lining
cc and for treatment of disturbances in fertility, contraception of
cc pregnancy. The present sequence represents the specifically claimed
cc TGF-beta monomeric protein MP52, from the present invention.
xx
sq Sequence: 501 AA;

Query Match 99.4%; Score 645; Ids 19; Length 501;
Best Local Similarity 99.2%; Prod. No. 5,96 59;
Matches 118; Conserved 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLATRGKRRSKNIKARCSKALHVNFKIMQMDWLTATLEYAFHCEGLPEPPLRSHLF 60
ID 483 PLATRGKRRSKNIKARCSKALHVNFKIMQMDWLTATLEYAFHCEGLPEPPLRSHLF 60
QY 61 PTNHAVTQTLNNSMDPESTPTACVPTREISPLSTLFTDSANNVVKQYELMVVESGGR 119
ID 443 PTNHAVTQTLNNSMDPESTPTACVPTREISPLSTLFTDSANNVVKQYELMVVESGGR 119
ID 443 PTNHAVTQTLNNSMDPESTPTACVPTREISPLSTLFTDSANNVVKQYELMVVESGGR 119

Search completed: March 26, 2002, 06:10:15
Job time: 74 sec

cc dental implants, neural tissue including CNS tissue and neuroepithelial
cc situations, tissue of the sensory system, liver, pancreas, cardiac,
cc blood vessels, renal, uterine and thyroid tissue, skin, mucous membrane,
cc endothelium, epithelium, for promotion or induction of nerve growth,
cc tissue regeneration, and/or for treatment of wound healing including ulcers, burns,
cc injuries of skin grafts, induction of proliferation of progenitor cells
cc or bone marrow cells, for maintenance of a state of proliferation or
cc differentiation, for treatment or preservation of tissue or cells for
cc organ or tissue transplantation, for integrity of osteointegration lining
cc and for treatment of disturbances in fertility, contraception of
cc pregnancy. The present sequence represents the specifically claimed
cc TGF-beta monomeric protein MP52, from the present invention.
xx
sq Sequence: 501 AA;

Query Match 99.4%; Score 645; Ids 19; Length 501;
Best Local Similarity 99.2%; Prod. No. 5,96 59;
Matches 118; Conserved 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLATRGKRRSKNIKARCSKALHVNFKIMQMDWLTATLEYAFHCEGLPEPPLRSHLF 60
ID 483 PLATRGKRRSKNIKARCSKALHVNFKIMQMDWLTATLEYAFHCEGLPEPPLRSHLF 60
QY 61 PTNHAVTQTLNNSMDPESTPTACVPTREISPLSTLFTDSANNVVKQYELMVVESGGR 119
ID 443 PTNHAVTQTLNNSMDPESTPTACVPTREISPLSTLFTDSANNVVKQYELMVVESGGR 119
ID 443 PTNHAVTQTLNNSMDPESTPTACVPTREISPLSTLFTDSANNVVKQYELMVVESGGR 119

Search completed: March 26, 2002, 06:10:15
Job time: 74 sec

cc dental implants, neural tissue including CNS tissue and neuroepithelial
cc situations, tissue of the sensory system, liver, pancreas, cardiac,
cc blood vessels, renal, uterine and thyroid tissue, skin, mucous membrane,
cc endothelium, epithelium, for promotion or induction of nerve growth,
cc tissue regeneration, and/or for treatment of wound healing including ulcers, burns,
cc injuries of skin grafts, induction of proliferation of progenitor cells
cc or bone marrow cells, for maintenance of a state of proliferation or
cc differentiation, for treatment or preservation of tissue or cells for
cc organ or tissue transplantation, for integrity of osteointegration lining
cc and for treatment of disturbances in fertility, contraception of
cc pregnancy. The present sequence represents the specifically claimed
cc TGF-beta monomeric protein MP52, from the present invention.
xx
sq Sequence: 501 AA;

Query Match 99.4%; Score 645; Ids 19; Length 501;
Best Local Similarity 99.2%; Prod. No. 5,96 59;
Matches 118; Conserved 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLATRGKRRSKNIKARCSKALHVNFKIMQMDWLTATLEYAFHCEGLPEPPLRSHLF 60
ID 483 PLATRGKRRSKNIKARCSKALHVNFKIMQMDWLTATLEYAFHCEGLPEPPLRSHLF 60
QY 61 PTNHAVTQTLNNSMDPESTPTACVPTREISPLSTLFTDSANNVVKQYELMVVESGGR 119
ID 443 PTNHAVTQTLNNSMDPESTPTACVPTREISPLSTLFTDSANNVVKQYELMVVESGGR 119
ID 443 PTNHAVTQTLNNSMDPESTPTACVPTREISPLSTLFTDSANNVVKQYELMVVESGGR 119

Search completed: March 26, 2002, 06:10:15
Job time: 74 sec

cc dental implants, neural tissue including CNS tissue and neuroepithelial
cc situations, tissue of the sensory system, liver, pancreas, cardiac,
cc blood vessels, renal, uterine and thyroid tissue, skin, mucous membrane,
cc endothelium, epithelium, for promotion or induction of nerve growth,
cc tissue regeneration, and/or for treatment of wound healing including ulcers, burns,
cc injuries of skin grafts, induction of proliferation of progenitor cells
cc or bone marrow cells, for maintenance of a state of proliferation or
cc differentiation, for treatment or preservation of tissue or cells for
cc organ or tissue transplantation, for integrity of osteointegration lining
cc and for treatment of disturbances in fertility, contraception of
cc pregnancy. The present sequence represents the specifically claimed
cc TGF-beta monomeric protein MP52, from the present invention.
xx
sq Sequence: 501 AA;

Query Match 99.4%; Score 645; Ids 19; Length 501;
Best Local Similarity 99.2%; Prod. No. 5,96 59;
Matches 118; Conserved 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLATRGKRRSKNIKARCSKALHVNFKIMQMDWLTATLEYAFHCEGLPEPPLRSHLF 60
ID 483 PLATRGKRRSKNIKARCSKALHVNFKIMQMDWLTATLEYAFHCEGLPEPPLRSHLF 60
QY 61 PTNHAVTQTLNNSMDPESTPTACVPTREISPLSTLFTDSANNVVKQYELMVVESGGR 119
ID 443 PTNHAVTQTLNNSMDPESTPTACVPTREISPLSTLFTDSANNVVKQYELMVVESGGR 119
ID 443 PTNHAVTQTLNNSMDPESTPTACVPTREISPLSTLFTDSANNVVKQYELMVVESGGR 119

Search completed: March 26, 2002, 06:10:15
Job time: 74 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 26, 2002, 06:09:02 : Search time 12.55 Seconds
(without alignments)
213.478 Million cell updates/sec

Title: US-09-701-121-2
Perfect score: 645
Sequence: 1 PLATROCKRPSKNIKARCSK.....ANNVYKQVEMVSESGR 119
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22504292 residues
Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents-AA*
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2: /cqn2_6/ptodata/2/1aa/5B_00MB.pep.*
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4: /cqn2_6/ptodata/2/1aa/6B_00MB.pep.*
5: /cqn2_6/ptodata/2/1aa/PTCUS_COMB.pep.*
6: /cqn2_6/ptodata/2/1aa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	length	ID	Description
1	645	99.4	120	1 US-08-362-670B-4	Sequence 4, Appl
2	645	99.4	120	3 US-08-333-576C-4	Sequence 4, Appl
3	645	99.4	120	4 US-08-808-324-4	Sequence 4, Appl
4	645	99.4	120	5 PCT-US94-14030A-4	Sequence 4, Appl
5	645	99.4	401	3 US-08-289-222E-3	Sequence 3, Appl
6	645	99.4	401	4 US-09-054-536B-3	Sequence 3, Appl
7	645	99.4	501	2 US-08-288-508C-2	Sequence 2, Appl
8	640	98.6	119	1 US-08-453-559-13	Sequence 13, Appl
9	640	98.6	119	4 US-09-145-060-13	Sequence 13, Appl
10	640	98.6	119	5 PCT-US94-00457-13	Sequence 13, Appl
11	640	98.6	495	1 US-08-455-559-10	Sequence 10, Appl
12	640	98.6	495	4 US-09-145-060-10	Sequence 10, Appl
13	640	98.6	495	5 PCT-US94-00457-10	Sequence 10, Appl
14	559	86.1	102	1 US-08-345-584C-51	Sequence 51, Appl
15	559	86.1	102	2 US-08-288-508C-13	Sequence 13, Appl
16	559	86.1	102	3 US-08-289-222E-22	Sequence 22, Appl
17	559	86.1	102	4 US-09-054-536B-22	Sequence 22, Appl
18	543	83.7	119	1 US-08-581-529B-7	Sequence 7, Appl
19	543	83.7	119	3 US-09-097-616-7	Sequence 7, Appl
20	543	83.7	119	5 PCT-US94-07762-7	Sequence 7, Appl
21	543	83.7	134	1 US-08-581-529B-6	Sequence 6, Appl
22	543	83.7	134	3 US-09-097-616-6	Sequence 6, Appl
23	543	83.7	134	5 PCT-US94-07762-6	Sequence 6, Appl
24	540	83.2	321	1 US-08-362-670B-26	Sequence 26, Appl
25	540	83.2	321	3 US-08-333-576C-26	Sequence 26, Appl
26	540	83.2	321	4 US-08-808-324-26	Sequence 26, Appl
27	540	83.2	321	5 PCT-US94-14030A-26	Sequence 26, Appl

28	548	82.9	263	1 US-08-362-670B-42	Sequence 42, Appl
29	548	82.9	263	3 US-08-333-576C-42	Sequence 42, Appl
30	548	82.9	263	4 US-08-808-324-42	Sequence 42, Appl
31	548	82.9	263	5 PCT-US94-14030A-42	Sequence 42, Appl
32	494	76.1	129	1 US-08-360-914B-15	Sequence 15, Appl
33	494	76.1	129	1 US-08-741-589A-13	Sequence 13, Appl
34	494	76.1	294	1 US-08-362-670B-2	Sequence 2, Appl
35	494	76.1	294	3 US-08-333-576C-2	Sequence 2, Appl
36	494	76.1	294	4 US-08-808-324-2	Sequence 2, Appl
37	494	76.1	294	5 PCT-US94-14030A-2	Sequence 2, Appl
38	494	76.1	388	1 US-08-362-670B-34	Sequence 34, Appl
39	494	76.1	388	3 US-08-333-576C-34	Sequence 34, Appl
40	494	76.1	388	4 US-08-808-324-34	Sequence 34, Appl
41	494	76.1	388	5 PCT-US94-14030A-34	Sequence 34, Appl
42	494	76.1	411	1 US-08-362-670B-28	Sequence 28, Appl
43	494	76.1	411	3 US-08-333-576C-28	Sequence 28, Appl
44	494	76.1	411	4 US-08-808-324-28	Sequence 28, Appl
45	494	76.1	411	5 PCT-US94-14030A-28	Sequence 28, Appl

ALIGNMENTS

RESUL1 1
US-08-362-670B-4
: Sequence 4, Application US/08362670B
: Patent No. 5658882
: GENERAL INFORMATION:
: APPLICANT: Celesteo, Anthony J.
: APPLICANT: Wozney, John
: APPLICANT: Rosen, Vicki A.
: APPLICANT: Wolfman, Neil
: APPLICANT: Ihmsen, Gerald H.
: APPLICANT: Melton, Douglas A.
: TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
: NUMBER OF SEQUENCES: 37
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: GENETICS INSTITUTE, INC.
: STREET: 87 CambridgePark Drive
: CITY: Cambridge
: STATE: Massachusetts
: COUNTRY: USA
: ZIP: 02140
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/362,670B
: FILING DATE: December 22, 1994
: CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
: NAME: Lazar, Steven R.
: REGISTRATION NUMBER: 32,618
: REFERENCE/INVENT NUMBER: 5202-D
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 617 498-8260
: TELEFAX: 617 876-5851
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 120 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-362-670B-4

Query Match 99.4% Score 645 DB 1 Length 120

Best Local Similarity 99.2% Pred. No. 9,36-65

Matches 119 Conservative 0 Mismatches 1 Labels 0 Gaps

QY 1 PLATROCKRPSKNIKARCSKALHVNFKMGWIDWITAPLEYAFHFGCTEPLRSIHL 60

DB 2 PLATPGKRSKNLKARSRKALHVNFKMGWMDWMTAPLEYEAFBGLTFFPLRSHE 61
 QY 61 PINHAVIQTLMNSMIPSTPTACVPTPLSPSTISLFTUSANNVVKQYEDMVVVSQGR 119
 DB 62 PINHAVIQTLMNSMIPSTPTCCVPTPLSPSTISLFTUSANNVVKQYEDMVVVSQGR 120

RESULT 2

US 08 343 5760 4
 ? Sequence 4, Application US/083435760
 ? Patent No. 6027919
 ? GENERAL INFORMATION:
 ? APPLICANT: Celvesto, Anthony J.
 ? APPLICANT: Wozniak, John
 ? APPLICANT: Rosen, Vicki A.
 ? APPLICANT: Wellman, Gerald H.
 ? APPLICANT: Thomson, Douglas A.
 ? APPLICANT: Melton, Douglas A.
 ? TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
 ? NUMBER OF SEQUENCES: 47
 ? CORRESPONDENCE ADDRESS:
 ? ADDRESSEE: GENETICS INSTITUTE, INC.
 ? STREET: 87 Cambridgepark Drive
 ? CITY: Cambridge
 ? STATE: Massachusetts
 ? COUNTRY: USA
 ? ZIP: 02140
 ? COMPUTER READABLE FORM:
 ? MEDIUM TYPE: Floppy disk
 ? COMPUTER: IBM PC compatible
 ? OPERATING SYSTEM: PC-DOS/MS-DOS
 ? SOFTWARE: Patent In Release #1.0, Version #1.25
 ? CURRENT APPLICATION DATA:
 ? APPLICATION NUMBER: US/08/333,5760
 ? FILING DATE: No. 6027919/September 2, 1994
 ? CLASSIFICATION: 435
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: Lazar, Steven R.
 ? REGISTRATION NUMBER: 42,618
 ? REFERENCE/DOCKET NUMBER: 5202-B
 ? TELECOMMUNICATION INFORMATION:
 ? TELEPHONE: 617 498-8260
 ? TELEFAX: 617 876-5851
 ? INFORMATION FOR SEQ ID NO: 4:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 120 amino acids
 ? TYPE: amino acid
 ? TOPOLOGY: linear
 ? MOLECULE TYPE: protein
 ? US 08 343 5760 4

Query Match: 99.4% Score 645; DB 4; Length 120;
 Best Local Similarity 99.2% Pred. No. 9, 40-65;
 Matches 118; conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLATPGKRSKNLKARSRKALHVNFKMGWMDWMTAPLEYEAFBGLTFFPLRSHE 60
 DB 2 PLATPGKRSKNLKARSRKALHVNFKMGWMDWMTAPLEYEAFBGLTFFPLRSHE 61
 QY 61 PINHAVIQTLMNSMIPSTPTACVPTPLSPSTISLFTUSANNVVKQYEDMVVVSQGR 119
 DB 62 PINHAVIQTLMNSMIPSTPTCCVPTPLSPSTISLFTUSANNVVKQYEDMVVVSQGR 120

RESULT 3

US 08-808-424-4
 ? Sequence 4, Application US/08080424
 ? Patent No. 6204872
 ? GENERAL INFORMATION:
 ? APPLICANT: Celvesto, Anthony J.
 ? APPLICANT: Wozniak, John

? APPLICANT: Rosen, Vicki A.
 ? APPLICANT: Wellman, Gerald H.
 ? APPLICANT: Thomson, Douglas A.
 ? APPLICANT: Melton, Douglas A.
 ? TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
 ? NUMBER OF SEQUENCES: 45
 ? CORRESPONDENCE ADDRESS:
 ? ADDRESSEE: GENETICS INSTITUTE, INC.
 ? STREET: 87 Cambridgepark Drive
 ? CITY: Cambridge
 ? STATE: Massachusetts
 ? COUNTRY: USA
 ? ZIP: 02140
 ? COMPUTER READABLE FORM:
 ? MEDIUM TYPE: Floppy disk
 ? COMPUTER: IBM PC compatible
 ? OPERATING SYSTEM: PC-DOS/MS-DOS
 ? SOFTWARE: Patent In Release #1.0, Version #1.25
 ? CURRENT APPLICATION DATA:
 ? APPLICATION NUMBER: US/08/808,424
 ? FILING DATE: November
 ? CLASSIFICATION: 514
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: Lazar, Steven R.
 ? REGISTRATION NUMBER: 42,618
 ? REFERENCE/DOCKET NUMBER: 5202-B
 ? TELECOMMUNICATION INFORMATION:
 ? TELEPHONE: 617 498-8260
 ? TELEFAX: 617 876-5851
 ? INFORMATION FOR SEQ ID NO: 4:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 120 amino acids
 ? TYPE: amino acid
 ? TOPOLOGY: linear
 ? MOLECULE TYPE: protein
 ? US 08 808 424 4

Query Match: 99.4% Score 645; DB 4; Length 120;
 Best Local Similarity 99.2% Pred. No. 9, 40-65;
 Matches 118; conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLATPGKRSKNLKARSRKALHVNFKMGWMDWMTAPLEYEAFBGLTFFPLRSHE 60
 DB 2 PLATPGKRSKNLKARSRKALHVNFKMGWMDWMTAPLEYEAFBGLTFFPLRSHE 61
 QY 61 PINHAVIQTLMNSMIPSTPTACVPTPLSPSTISLFTUSANNVVKQYEDMVVVSQGR 119
 DB 62 PINHAVIQTLMNSMIPSTPTCCVPTPLSPSTISLFTUSANNVVKQYEDMVVVSQGR 120

RESULT 4

US 94 140 400 4
 ? Sequence 4, Application US/94140400A
 ? GENERAL INFORMATION:
 ? APPLICANT: GENETICS INSTITUTE, INC.
 ? APPLICANT: PRESIDENT AND FELLOWS OF HARVARD COLLEGE
 ? TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
 ? NUMBER OF SEQUENCES: 45
 ? CORRESPONDENCE ADDRESS:
 ? ADDRESSEE: GENETICS INSTITUTE, INC.
 ? STREET: 87 Cambridgepark Drive
 ? CITY: Cambridge
 ? STATE: Massachusetts
 ? COUNTRY: USA
 ? ZIP: 02140
 ? COMPUTER READABLE FORM:
 ? MEDIUM TYPE: Floppy disk
 ? COMPUTER: IBM PC compatible
 ? OPERATING SYSTEM: PC-DOS/MS-DOS
 ? SOFTWARE: Patent In Release #1.0, Version #1.25
 ? CURRENT APPLICATION DATA:
 ? APPLICATION NUMBER: US/94/140400A

FILING DATE: Herewith
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/164,104
 FILING DATE: 07-DEC-1993
 APPLICATION NUMBER: US 08/217,780
 FILING DATE: 25-MAR-1994
 APPLICATION NUMBER: US 08/444,576
 FILING DATE: 02-NOV-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Lazar, Steven R.
 REGISTRATION NUMBER: 42,618
 REFERENCE/DOCKET NUMBER: 52020-PCT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617 498 5260
 TELEFAX: 617 876-5851
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 120 amino acids
 TYPE: amino acid
 TOPOLOGY: Linear
 MOLECULE TYPE: protein
 PCT-US94-14030A-4

Query Match 99.4%; Score 645; DB 5; Length 120;
 Best Local Similarity 99.2%; Pred. No. 9,40-65;
 Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 PLATROCKRKPSKNIKARCSRKALHVNFKMGWDDWIIAPLEYAFHCEPLRSHLE 60
 DB 2 PLATROCKRKPSKNIKARCSRKALHVNFKMGWDDWIIAPLEYAFHCEPLRSHLE 61
 QY 61 PTHAVIQTILMSMDPESTPTACVPTRLSPISILFIDSANNVVKOYEDMVVESGCR 119
 DB 62 PTHAVIQTILMSMDPESTPTACVPTRLSPISILFIDSANNVVKOYEDMVVESGCR 120

RESULT 5
 US-08-289-222E-4
 Sequence 3, Application US/08289222E
 Patent No. 6120760
 GENERAL INFORMATION:
 APPLICANT: HOTTEN, GERTRUD
 APPLICANT: NEIDHARDT, HELGE
 APPLICANT: RECHTOLD, ROLF
 APPLICANT: POHL, JENS
 TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS OF THE TGF B
 NUMBER OF SEQUENCES: 53
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: NIKALDO, MARMELESTEIN, MURRAY & ORAM
 STREET: 655 FIFTEENTH STREET, N. W., G STREET LOBBY,
 STREET: SUITE 400
 CITY: WASHINGTON
 STATE: DC
 COUNTRY: USA
 ZIP: 20005-5701
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/289,222E
 FILING DATE: 25-AUG-1999
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/289,222
 FILING DATE: 12-AUG-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: DE P 44 23 190.4
 FILING DATE: 07-JUL-1994

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: EP0 92102424.8
 FILING DATE: 12-FEB-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/EP93/00450
 FILING DATE: 12-FEB-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: KITTIS, MONICA CHIN
 REGISTRATION NUMBER: 36,105
 REFERENCE/DOCKET NUMBER: P564-4021
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202/678-5000
 TELEFAX: 202/638-4810
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 401 amino acids
 TYPE: amino acid
 STRANDEDNESS: Single
 TOPOLOGY: Linear
 MOLECULE TYPE: protein
 US-08-289-222E-3

Query Match 99.4%; Score 645; DB 4; Length 401;
 Best Local Similarity 99.2%; Pred. No. 4,2e-64;
 Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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 DB 283 PLATROCKRKPSKNIKARCSRKALHVNFKMGWDDWIIAPLEYAFHCEPLRSHLE 442
 QY 61 PTHAVIQTILMSMDPESTPTACVPTRLSPISILFIDSANNVVKOYEDMVVESGCR 119
 DB 343 PTHAVIQTILMSMDPESTPTACVPTRLSPISILFIDSANNVVKOYEDMVVESGCR 401

RESULT 6
 US-09-054-524E-4
 Sequence 3, Application US/09054526B
 Patent No. 6147560
 GENERAL INFORMATION:
 APPLICANT: HOTTEN, GERTRUD
 APPLICANT: NEIDHARDT, HELGE
 APPLICANT: RECHTOLD, ROLF
 APPLICANT: POHL, JENS
 TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL
 TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS
 NUMBER OF SEQUENCES: 53
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: NIKALDO, MARMELESTEIN, MURRAY & ORAM LLP
 STREET: 655 FIFTEENTH STREET, N. W., G STREET LOBBY,
 STREET: SUITE 330
 CITY: WASHINGTON
 STATE: DC
 COUNTRY: USA
 ZIP: 20005-5701
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/054,526B
 FILING DATE: 03-AUG-1998
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/289,222
 FILING DATE: 12-AUG-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: DE P 44 23 190.4
 FILING DATE: 01-JUL-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: EP0 92102424.8
 FILING DATE: 12-FEB-1992

```

? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: PCT/EP94/00450
? FILING DATE: 12-FEB-1994
? ATTORNEY/AGENT INFORMATION:
? NAME: KLITS, MONICA CHIN
? REGISTRATION NUMBER: 46,105
? REFERENCE/DRAWING NUMBER: 1564 8005
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 202/638-5000
? TELEFAX: 202/638-4810
? INFORMATION FOR SEQ ID NO: 4:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 401 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? US-09-054 526B-4
?
? Query Match
? Best Local Similarity 99.4% Score 645; DB 4; Length 401;
? Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
?
? QY 1 PLATQGRKRSKNLKARSRKALHVNFKIMWDMWDLAPLEYEAFHCEGLCEPLRSKLE 60
? DB 283 PLATQGRKRSKNLKARSRKALHVNFKIMWDMWDLAPLEYEAFHCEGLCEPLRSKLE 342
?
? QY 61 PTNHAVIQTLNMSMDPESTPTACVPTKSPISLTFDUSANNVYKQYEMVVSQGR 119
? DB 443 PTNHAVIQTLNMSMDPESTPTACVPTKSPISLTFDUSANNVYKQYEMVVSQGR 401
?
? RESULT 7
? US-09-288 508C-2
? Sequence 2; Application US/08288508C
? Patent No. 5994694
? GENERAL INFORMATION:
? APPLICANT: HUGO, Gottfried
? APPLICANT: Neidhardt, Helge
? APPLICANT: Fontana, Michael
? TITLE OF INVENTION: NEW GROWTH/DIFFERENTIATING FACTOR OF
? NUMBER OF SEQUENCES: 40
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Nikaido, Marmelstein, Murray & Gram LLP
? STREET: 655 Fifteenth Street N.W. Suite 340
? CITY: Washington
? STATE: D.C.
? COUNTRY: U.S.A.
? ZIP: 20005 5701
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC DOS/MS DOS
? SOFTWARE: Patent Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/288,508C
? FILING DATE: 10-AUG-1994
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: DE P 44 26 829.4
? FILING DATE: 10-AUG-1994
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: DE P 44 18 222.8
? FILING DATE: 25-MAY-1994
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: DE P 44 20 157.5
? FILING DATE: 09-JUN-1994
? ATTORNEY/AGENT INFORMATION:
? NAME: JAHNS, Kristina M.
? REGISTRATION NUMBER: P-41,092
? REFERENCE/DRAWING NUMBER: 1564 4019

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? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (202)638-5000
? TELEFAX: (202)638-4810
? INFORMATION FOR SEQ ID NO: 2:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 501 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? US-08-288 508C-2
?
? Query Match
? Best Local Similarity 99.4% Score 645; DB 2; Length 501;
? Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
?
? QY 1 PLATQGRKRSKNLKARSRKALHVNFKIMWDMWDLAPLEYEAFHCEGLCEPLRSKLE 60
? DB 483 PLATQGRKRSKNLKARSRKALHVNFKIMWDMWDLAPLEYEAFHCEGLCEPLRSKLE 442
?
? QY 61 PTNHAVIQTLNMSMDPESTPTACVPTKSPISLTFDUSANNVYKQYEMVVSQGR 119
? DB 443 PTNHAVIQTLNMSMDPESTPTACVPTKSPISLTFDUSANNVYKQYEMVVSQGR 401
?
? RESULT 8
? US-08-455 559-13
? Sequence 13; Application US/08455559
? Patent No. 5601014
? GENERAL INFORMATION:
? APPLICANT: DEE, SE JIN
? APPLICANT: HUYNH, THANH
? TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR 5
? NUMBER OF SEQUENCES: 27
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: SPENSLEY BORN JIHAS & LORILL
? STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
? CITY: LOS ANGELES
? STATE: CALIFORNIA
? COUNTRY: US
? ZIP: 90067
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC DOS/MS DOS
? SOFTWARE: Patent Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/455,559
? FILING DATE: 31-MAY-1995
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US-08/003,144
? FILING DATE: 12-JAN-1994
? ATTORNEY/AGENT INFORMATION:
? NAME: WETHERELL, JR., PH.D., JOHN R.
? REGISTRATION NUMBER: 41,678
? REFERENCE/DRAWING NUMBER: P42280
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 619/455-5100
? TELEFAX: 619-455-5110
? INFORMATION FOR SEQ ID NO: 13:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 119 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? IMMEDIATE SOURCE:
? CLONE: GDF 5
? FEATURE:
? NAME/KEY: protein
? LOCATION: 1-119
? US-08-455 559-13

```


CITY: LOS ANGELES
STATE: CALIFORNIA
COUNTRY: US
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,559
FILING DATE: 31-MAY 1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/003,144
FILING DATE: 12 JAN 1993
ATTORNEY/AGENT INFORMATION:
NAME: WETHERELL, JR, PH.D., JOHN R.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: 092,280
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/455-5100
TELEFAX: 619-455-5110
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 495 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
S-08-455-559-10

Query Match	98.48%	Score: 640	10k: 1	Length: 495
Global Similarity	98.48%	Prod. No.: 26,612		
Matches: 117	Conservative	Mismatches: 2	Indels: 0	Gaps: 0
QY	1	PLATQCKRQTSKNIKARCSSKALHVNEKMGMDWT	1	LALEFEAFHICLCEETTESHLE
	11	111111111111111111111111111111111111		111111111111111111111111111111111111
QB	477	PLANKQCKRQTSKNIKARCSSKALHVNEKMGMDWT	2	LALEFEAFHICLCEETTESHLE
	11	111111111111111111111111111111111111		111111111111111111111111111111111111
QY	61	PTNIAVQTLMNSMDQSTPTACVTRSPSLFPLDSANNVAVKQVEDMVAESGCR	1	119
	11	111111111111111111111111111111111111		111111111111111111111111111111111111
QB	447	PTNIAVQTLMNSMDQSTPTACVTRSPSLFPLDSANNVAVKQVEDMVAESGCR	1	495
	11	111111111111111111111111111111111111		111111111111111111111111111111111111

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1  RESULT 12
2  US-99 145 060-10
3  : Sequence 10, Application US/09145060
4  : Patent No. 6245896
5  :
6  : GENERAL INFORMATION:
7  :
8  : APPLICANT: Iac, Seidin
9  : APPLICANT: Buyuk, Thuth
10 : TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR 5
11 : NUMBER OF SEQUENCES: 27
12 : CORRESPONDENCE ADDRESS:
13 :
14 : ADDRESSEE: Fish & Richardson, P.C.
15 : STREET: 4225 Executive Square, Suite 1400
16 : CITY: La Jolla
17 : STATE: CA
18 : COUNTRY: USA
19 :
20 : ZIP: 92037
21 :
22 : COMPUTER RELEASABLE FORM:
23 : MEDIUM TYPE: Diskette
24 : COMPUTER: IBM Compatible
25 :
26 : OPERATING SYSTEM: Windows95
27 :
28 : SOFTWARE: FastSeq for Windows Version 2.0
29 : CURRENT APPLICATION DATA:
30 : APPLICATION NUMBER: US/09/145,060
31 : FILING DATE:
32 :
33 : PRIOR APPLICATION DATA:
34 : APPLICATION NUMBER: 08/455,459
35 : FILING DATE: 31-MAY-1995
36 : APPLICATION NUMBER: 08/008,144

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1  FILLING DATE: 12 JAN 1994
2
3  ATTORNEY/AGENT INFORMATION:
4  NAME: Lisa A. Bailo, Ph.D.
5  REGISTRATION NUMBER: 58, 447
6  REFERENCE NUMBER: 07265/05,001
7
8  TELECOMMUNICATION INFORMATION:
9  TELEPHONE: 619/678 5070
10  TELEFAX: 619/678 5099
11  INFORMATION FOR SEQ ID NO: 10:
12  SEQUENCE CHARACTERISTICS:
13  LENGTH: 495 amino acids
14  TYPE: amino acid
15  TOPOLOGY: linear
16
17  MOLECULE TYPE: protein
18  FRAGMENT TYPE: internal
19
20  US-09 145,066-10
21
22  Query Match 98.4%; Score 640; DB 4; Length 495;
23  Best Local Similarity 98.4%;
24  Matches 117; Conserved 10; Mismatch 0; Gaps
25
26  QY 1 PLAIKRGKRSKNIKAKRSKKALHVNFKIMQIMQIMLAPLEEFAPHFEGLPEFLPSHLE 495
27  DB 377 PLAIKRGKRSKNIKAKRSKKALHVNFKIMQIMQIMLAPLEEFAPHFEGLPEFLPSHLE 495
28
29  QY 61 PNIHVIQTILNNSMDDESTPTACVPTRELSPTSLFLEIUSANNVVVYKVEYDQVVFSSQGR 119
30  DB 447 PNIHVIQTILNNSMDDESTPTPTCCVPTRELSPTSLFLEIUSANNVVVYKVEYDQVVFSSQGR 495

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RESULT 14
 : Sequence ID, Application PC/T059400657
 : GENERAL INFORMATION:
 : APPLICANT: SPATIN LEE
 : APPLICANT: IOWAN, THOMAS
 : TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR 5
 : NUMBER OF SEQUENCES: 27
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: STENSTLEY DORN, JONAS & LORETZ
 : STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
 : CITY: LOS ANGELES
 : STATE: CALIFORNIA
 : COUNTRY: US
 : ZIP: 90067
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC DOS/MS DOS
 : SOFTWARE: Patent In Release #1.0, Version #1.25,
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: PAT/US94/00657
 : FILING DATE: 1/12/94
 : CLASSIFICATION:
 : ATTORNEY/AGENT INFORMATION:
 : NAME: WETHERELL, JR, PH.D., JOHN R.
 : REGISTRATION NUMBER: 41,678
 : REFERENCE/PROCKET NUMBER: F4256, CIP OF P42280
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 619/455, 5100
 : TELEFAX: 619, 455, 5110
 : INFORMATION FOR SEQ ID NO: 10:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 455 amino acids
 : TYPE: amino acid
 : TOPOLOGY: linear
 : MOLECULE TYPE: protein
 : CT 0594 00657 10

Query Match	Score	Length
98.6%	640	108
98.3%	640	20


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RESULT 7
S52408
C:Species: Strongylocentrotus purpuratus
C:Date: 06-May-1995 #sequence_revision 21-Jul-1995 #text_change 20-Sep-1999
C:Accession: S52408
R:ponce, M.R.; Nicol, J.L.; Davidson, E.H.
submitted to the EMBL Data Library, February 1995
A:Description: SpVR1, a member of the transforming growth factor-beta superfamily expressed
A:Reference number: S52408
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-461 #LEN>
A:Cross-references: EMBL:Z48313; NID:q673496; PID:q674497
C:Superfamily: inhibin

Query Match 53.5% Score 353.5; DB 2; Length 461;
Best Local Similarity 54.3%; Pred. No. 26-28;
Matches 63; Conservative 19; Mismatches 32; Indels 19; Gaps 2;

QY 3 ATRQ--CKRPSK-----NIKAK*SRKALHVNFKDMGWIIIAILEYE 43
DB 426 ATRQKGGRRKRPDINDIASRDSASSLSDWCKRKNI*FVNFDLQWGVIIAIPGYV 485
QY 44 AFHCERLFEPLRSHLEPTTACVPTRLSPISLIFDSANNV 103
DB 486 AFYQGECAFLNHNATNHAIVQTLVHMSSHVFPQCAPIKLSPIILVYDIDSRNV 445
QY 104 VYQVDEMVSQGG 118
DB 446 VLKKYKNVVRACGG 460

RESULT 8
S37073
bone morphogenetic protein 2 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Jul-1999
C:Accession: S37073
R:Feng, J.Q.; Chen, D.; Feng, M.; Harris, M.A.; Mundy, G.R.; Harris, S.E.
submitted to the EMBL Data Library, September 1993
A:Description: cDNA sequence of total rat calvarial osteoblast bone morphogenetic protein
A:Reference number: S37073
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-394 #LEN>
A:Cross-references: EMBL:Z25868; NID:q347950; PID:CAAB1088.1; PID:q347951
C:Superfamily: inhibin

Query Match 53.5% Score 347; DB 2; Length 394;
Best Local Similarity 54.3%; Pred. No. 26-28;
Matches 63; Conservative 17; Mismatches 34; Indels 2; Gaps 2;

QY 5 RQKK-RPSKNIKARC*SRKALHVNFKDMGWIIIAILEYEAFHCERLFEPLRSHLEPTN 63
DB 279 RQAKRKRKRKSSCKRHPLVYDFSDVGNWDWIVAFPGYHAFYCGEGFPFLAHILNSTN 338
QY 64 HAVIQTLNNSMDPSTPTACVPTRLSPISLIFDSANNVVKQYEDMVVESGCR 119
DB 439 HAVIQTLNNSVN-SKIPKKA*VPTLSALSMLYLDENEKVKVILKNYQDMVVEG*GCR 393

RESULT 9
S45455
bone morphogenetic protein-2 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 10-Dec-1994 #sequence_revision 17-Nov-1995 #text_change 03-May-1996
C:Accession: S45455

```

```

R:Feng, J.Q.; Harris, M.A.; Glosch-Glaudbury, N.; Feng, M.; Mundy, G.R.; Harris, S.E.
Biochim. Biophys. Acta 1218, 221-224, 1994
A:Title: Structure and sequence of mouse bone morphogenetic protein-2 gene (BMP-2); c
A:Reference number: S45455; MUID:94284845
A:Accession: S45455
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-394 #LEN>
C:Superfamily: inhibin

Query Match 53.5% Score 347; DB 2; Length 394;
Best Local Similarity 54.3%; Pred. No. 26-28;
Matches 63; Conservative 17; Mismatches 34; Indels 2; Gaps 2;

QY 5 RQKK-RPSKNIKARC*SRKALHVNFKDMGWIIIAILEYEAFHCERLFEPLRSHLEPTN 63
DB 280 RQAKRKRKRKSSCKRHPLVYDFSDVGNWDWIVAFPGYHAFYCGEGFPFLAHILNSTN 339
QY 64 HAVIQTLNNSMDPSTPTACVPTRLSPISLIFDSANNVVKQYEDMVVESGCR 119
DB 439 HAVIQTLNNSVN-SKIPKKA*VPTLSALSMLYLDENEKVKVILKNYQDMVVEG*GCR 394

RESULT 10
BMH02
bone morphogenetic protein 2 precursor - human
N:Alternate names: bone morphogenetic protein 2A; rhBMP2
C:Species: Homo sapiens (man)
C:Date: 16-Sep-1992 #sequence_revision 03-Aug-1995 #text_change 18-Jun-1999
C:Accession: B37278; PC2178
R:Wozney, J.M.; Rosen, V.; Celeste, A.J.; Mitsock, L.M.; Whitters, M.J.; Krieger, R.W.;
Science 242, 1528-1534, 1988
A:Title: Novel regulators of bone formation: molecular clones and activities.
A:Reference number: A37278; MUID:89072730
A:Accession: B37278
A:Molecule type: mRNA
A:Residues: 1-396 #LEN>
A:Cross-references: GB:M22489; NID:q179501; PID:AAA51834.1; PID:q179502
R:Ishida, N.; Tsujimoto, M.; Kanaya, I.; Shimamura, A.; Tsurucka, N.; Kodama, S.; Kat
J. Biochem. 115, 279-285, 1994
A:Title: Expression and characterization of human bone morphogenetic protein-2 in sil
A:Reference number: PC2178; MUID:94266754
A:Accession: PC2178
A:Molecule type: protein
A:Residues: 290-295, 297-304 #ISH>
A:Experimental source: cell line BOM0-15A1ic
R:Kathore, S.; Hammerstone, K.M.; Dausorean, S.; Butler, L.J.
Protein Sci. 4(Suppl.2), 443S, 1995
A:Title: N-terminal isoforms of recombinant human bone morphogenetic protein (rhBMP-2
A:Reference number: A56729
A:Contents: annotation
A:Note: determination of amino acids of mature forms; dimers with long term chains have
C:Comment: this hormone is capable of inducing bone formation at ectopic morphological
C:Genetics:
A:Gene: GBB:BMP2A
A:Cross-references: GDB:125204; OMIM:112261
A:Map position: 20p12-20p12
C:Complex: homodimer; disulfide linked
C:Superfamily: inhibin
C:Keywords: bone; dimer; glycoprotein; pyroglutamic acid
F:1-23/Domain: signal sequence #status predicted -SIC>
F:24-265/Domain: propeptide #status predicted -SIC>
F:266-396/Product: bone morphogenetic protein 2; #status predicted -SIC>
F:283-396/Product: bone morphogenetic protein 2; #status predicted -SIC>
F:145,163,164,200/Binding site: carboxylate (Asn) (covalent) #status predicted -MAL>
F:283/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status expect
F:338/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 53.5% Score 347; DB 1; Length 396;
Best Local Similarity 54.3%; Pred. No. 26-28;
Matches 63; Conservative 17; Mismatches 34; Indels 2; Gaps 2;

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	1:	2:	Gaps:
Best local Similarity	48.7%	pred. No. 5, 4e-28;	
Matches	57;	Conservative	34; Indels
		24; Mismatches	34;

5 HQ*KRIS - KNI.KAKC\$KALHVNFKDMGWIOWI IAPLEYEAFHCFGLCEFFPLRSHLEPI 62

472 RHARRP1RKNHDDTCRRHS1VDFSDYGDWDW1VAP1GYDAYYCHGKCPFO1ADJENST 531

63 NHAVIQTILMNSMDPESTPTA'VPTRLSPISILFTISANNVVYKQYEDMVVESQ'NR 119

532 NHAVVOTI VNNNNPCKVDR ACCVPTOTI DSVAMI V' NIHASTAVI KNYJPMVWV' V' V' 5599

RESULT 15

XXXXXXXXXX

bone morphogenetic protein 2/1 precursor - African clawed frog

C. Species: *Xenopus laevis* (African clawed frog)

```

Date: 30 Sep-1994 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999

```

C; Accession: JH0688

R; Nishimatsu, S.; Suzuki, A.; Shoda, A.; Murakami, K.; Ijono, N.

Biochem. Biophys. Res. Commun. 186, 1487-1495, 1992

A: Title: Genes for bone morphogenetic proteins are differentially transcribed in early

A:Reference number: JH0687; MUID:92378616

A;Accession: JH0688

A: Molecule type: mRNA

A: Residues: 1-348 + NLS*

A:Residues: 1-398 + NLS
 A:Cross-references: (JB: X63425; NID: a64583; P1IN: CAA45019; 1- PID: a64584)

A:Cross-References: CB:X63423;
A:Experiment4 | source: oocyte

A; Experimental source:

Supernatural: Supernatural

Key words: glycoprotein
F: 285-398/Product; bone morphogenetic protein 211 #status predicted -MAT
F: 147,202,237,340/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

Query Match 52.9%; SCORE 343; LB 2; Length 398;

Best Local Similarity 53.48; Pred. No. 5, 3e-28;
Matches 62; Conservative 19; Mismatches 33; Indels 2; Gaps 2;

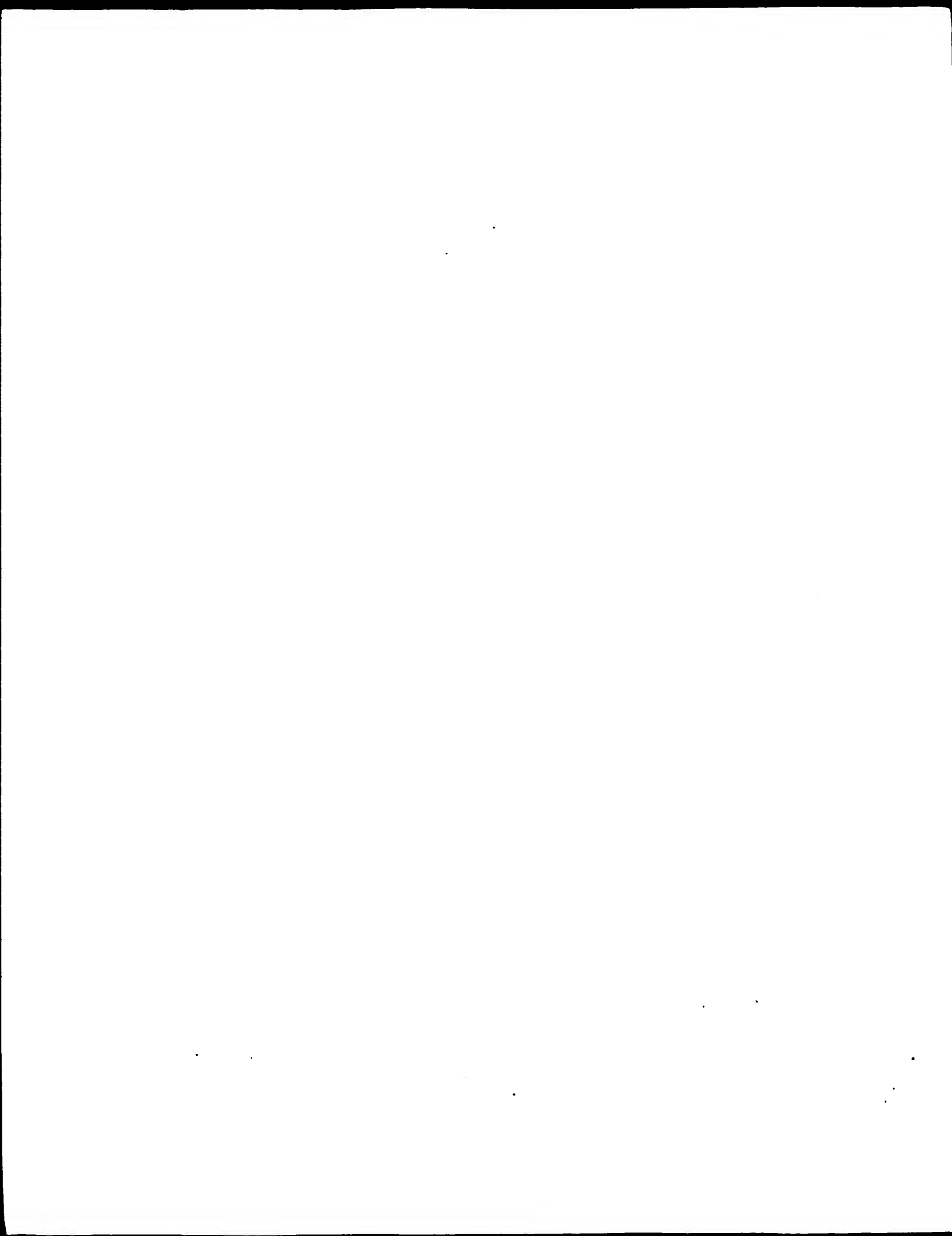
5 KQCK-RPSKNI.KARCSRKAL.HVNP.KDMGWTDWI IAPLEYEAFHCEGLCEFPPLRSHLEPTN 63

284 ROARKIKOKKRI KSSCBRII YVDESOMGWNW I VADBYUHAUYCHCEBPI AWI NSTN 243

64 HAVIOTIMNSMIDESTBPTACVPIRISPISEIFDSANNVVVKOYFIWVVSANVR 119

[illegible]

Search completed: March 26, 2002, 06:09:44
Job time: 42 sec



GenCore version 4.5
Copyright (c) 1993-2000 Compugen Ltd.

QM protein - protein search, using sw model

Run on: March 26, 2002, 06:09:47 ; Search time 22.3 seconds
(without alignments)
780,556 Million cell updates/sec

Title: us-09-701-121-2

Perfect score: 649

Sequence: 1 PLATROCKRPSKNIKARSR.....ANNVVYQVEMVMSVSGR 119

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 6%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SP_TREMBL_17:*

2: SP_Bacteria:*

3: SP_Fungi:*

4: SP_Human:*

5: SP_Invertebrate:*

6: SP_Mammal:*

7: SP_Misc:*

8: SP_Organelle:*

9: SP_Phage:*

10: SP_Plant:*

11: SP_Rodent:*

12: SP_Virus:*

13: SP_Vertebrate:*

14: SP_Unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length DB	ID	Description
1	637	98.2	500	13	Q9W630
2	587	90.4	324	13	Q9YBW9
3	563	86.7	257	13	Q42303
4	544.5	82.4	126	13	Q93573
5	527.5	81.3	261	13	Q9W630
6	527	81.2	413	13	Q9W630
7	524	80.7	399	13	Q9W753
8	524	80.7	412	13	Q12948
9	491	75.7	294	6	Q9BDW9
10	491	75.7	447	6	Q9BDW9
11	486	59.5	441	11	Q9YMY1
12	468.5	56.8	361	5	Q96504
13	468	56.7	204	5	Q9XZ59
14	466	56.4	411	5	Q90418
15	465	56.2	405	5	Q905B8
16	461	55.6	289	5	Q9XY08
17	459	55.3	417	5	Q9XY07
18	455.5	54.8	178	5	Q25211
19	454	54.5	67	6	Q02783

20	449.5	53.9	411	13	Q57573
21	449.7	53.9	411	13	Q93469
22	347	53.5	588	5	Q9V066
23	346	53.3	400	13	Q74818
24	346	53.3	400	13	Q91703
25	346	53.3	443	5	Q76851
26	444.5	53.1	411	13	Q14108
27	342.5	52.8	191	5	Q26468
28	342	52.7	373	13	Q90723
29	342	52.7	373	13	Q98950
30	342	52.7	400	13	Q57574
31	340	52.4	400	13	Q14107
32	338	52.1	614	5	Q91720
33	336.5	51.8	347	6	Q9M2V5
34	335	51.6	386	13	Q14109
35	335	51.6	424	13	Q9YGR7
36	334	51.5	301	5	Q97390
37	333	51.3	453	13	Q87373
38	330	50.8	177	4	Q9H512
39	330	50.8	314	13	Q91403
40	330	50.8	354	13	Q9YGV1
41	330	50.8	398	13	Q91816
42	325	50.1	432	13	Q91FF9
43	317.5	48.9	185	5	Q9GKA7
44	306.5	47.2	365	5	Q02424
45	306.5	47.2	365	5	Q76514

ALIGNMENTS

RESULT 1

Q9W630

AC Q9W630 PRELIMINARY: FR1: 500 AA.

BT 01-NEW-1999 (11FMBREL: 12, created)

BT 01-NEW-1999 (11FMBREL: 12, last sequence update)

BT 01-JUN-2001 (11FMBREL: 17, last annotation update)

DE GDF-5 PROTEIN.

GN GDF5.

OS Gallus gallus (chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neornithae; Galliformes; Phasianidae; Phasianinae; Gallus.

OX NCBI_LaXID:9931;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE:9914693; PubMed:10021348;

RA Francis-West P.H., Abdellattah A., Chou P., Allen C., Parish J., Lathier R., Allen S., MacPherson S., Layten F., Archer C.W.,

RI "Mechanisms of GDF-5 action during skeletal development";

RL Development 126:1305-1315(1999).

CC 1- SIMILARITY: TO THE TGF-BETA FAMILY.

DR EMBL: AF123489; AAC00451.1;

DR HSSP: P12643; 30MP.

DR InterPro: IPR002405; Inhibin.alpha.

DR InterPro: IPR001849; TGF-beta.

DR InterPro: IPR001111; IGFB_N.

DR Pfam: PF00019; TGF-beta: 1.

DR Pfam: PF00688; IGFB_propeptide: 1.

DR PRINTS: PK0060; INHIBINA.

DR ProDom: PD000357; TGF-beta: 1.

DR SMART: SM00204; TGF-beta: 1.

DR PROSITE: PS00250; IGFBETA: 1.

KW Glycoprotein.

SQ SEQUENCE 500 AA: 55962 MW: 108385A3119A598 CR664;

Query Match 98.2%; Score 637; DB 13; Length 500;

Best Local Similarity 97.5%; Pred. No. 176-64;

Matches 110; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 PLATROCKRPSKNIKARSRKALIVNEKDMWQWQW:119LLEYEAFHCTEGD:TEFLKSHLE 60

RESULTS	3
04-2-03	
119	PRELIMINARY; PRE; 257 AA.
AC	04-2-03;
DT	01 JAN 1998 (TEMPERATURE, 0% created)
101	01 JAN 1998 (TEMPERATURE, 0%, last software update)
101	01 JUN 2001 (TEMPERATURE, 17, last annotation update)
DE	CONFLICT (FRAGMENT).
UN	UNKNOWN.
GS	Braichydanio rerio (Zebrafish) (Zebra danio).
006	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
006	Agnostostomus; Neopterygii; Teleostei; Euteleostei; Euteleostomi;

[illegible]

KW Glycoprotein. 1 1
 FI NON-TER 126 AA: 14265 MW: CB824D280F44A394 CR664;
 SQ SEQUENCE

Query Match 82.4%; Score 534.5; DB 13; Length 126;
 Best Local Similarity 79.0%; Pred. No. 1,90-52;
 Matches 94; Conservative 13; Mismatches 11; Indels 1; Gaps 1;
 QY 2 LATRUCKR PSKNIKARSRKALHNPKDMGWIMLAPLEYEAFHCEGLCEPFLRSKLE 60
 DB 8 LAARSGRGGRKKAKTRCSRKPLHNFKELGWIMLAPLEYEAFHCEGLCEPFLRSKLE 67
 QY 61 PTNHAVIQTILMNSMDPESTPTACVPTKLSPTLSILFSDSANNVVKYQYEMVVESSGR 119
 DB 68 PTNHAIQTILMNSMDPESTPTSCCVSKLSPTLSILFSDSANNVVKYQYEMVVESSGR 126

RESULT 5
 QW6630
 ID QW6630 PRELIMINARY: PRI: 261 AA.
 AC QW6630
 DT 01-NOV-1999 (FEMBLrel. 12, Created)
 DT 01-NOV-1999 (FEMBLrel. 12, Last sequence update)
 DT 01-JUN-2001 (FEMBLrel. 17, Last annotation update)
 DE GROWTH/DIFFERENTIATION FACTOR 7 (FRAGMENT).
 GN GDF7.
 OS Brachydanio rerio (Zebrafish) (Zebra danio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
 CC Cypriniformes; Cyprinidae; Rasbora; Danio.
 OX NCBI_TaxID: 7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE 99148135; PubMed 16022976;
 RA Davidson A.J., Postlewait J.H., Yan Y.L., Bolet D.P., van Boren C.,
 RA Fournzier D., Celeste A.J., Crosier K.E., Grosier P.S.;
 RT "Isolation of zebrafish gdf7 and comparative genomic mapping of genes
 belonging to the growth/differentiation factor 5, 6, 7 subgroup of the
 RT IGF-beta superfamily."
 RL Genome Res. 9:121-129(1999).
 CC -1- SIMILARITY: TO THE IGF-BETA FAMILY.
 DR EMBL: AF113023; AAD20829.1; -.
 DR HSSP: P12643; 4RMP.
 DR InterPro: IPR002400; GF_cysknot.
 DR InterPro: IPR002405; Inhibin_alpha.
 DR InterPro: IPR001839; IGF-beta.
 DR Pfam: PF00019; IGF-beta; 1.
 DR PRINTS: PR00438; GFYSKNOT.
 DR PRINTS: PR00669; INHIBINA.
 DR ProDom: PD000457; IGF-beta; 1.
 DR SMART: SM00204; TGF; 1.
 DR PROSITE: PS00250; TGF_BETA; 1.
 KW Glycoprotein. 1 1
 FI NON-TER 261 AA: 29414 MW: 77346E977046A104 CR664;
 SQ SEQUENCE

Query Match 81.4%; Score 527.5; DB 13; Length 261;
 Best Local Similarity 76.0%; Pred. No. 2,70-52;
 Matches 95; Conservative 11; Mismatches 12; Indels 7; Gaps 1;
 QY 2 LATRUCKRPSKNIKARSRKALHNPKDMGWIMLAPLEYEAFHCEGLCEPFLRSKLE 54
 DB 147 LAGRGVGVPTSGGKGGRRKTRCSRKPLHNFKELGWIMLAPLEYEAFHCEGLCEP 196
 QY 55 LRSHLEPTNHAVIQTILMNSMDPESTPTACVPTKLSPTLSILFSDSANNVVKYQYEMVVE 114
 DB 147 LRSHLEPTNHAIQTILMNSMDPESTPTSCCVSKLSPTLSILFSDSANNVVKYQYEMVVE 256

QY 115 SAGGR 119
 DB 257 SAGGR 261

RESULT 6
 QW63N4
 ID QW63N4 PRELIMINARY: PRI: 413 AA.
 AC QW63N4
 DT 01-MAR-2001 (FEMBLrel. 16, Created)
 DT 01-MAR-2001 (FEMBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (FEMBLrel. 17, Last annotation update)
 DE GROWTH/DIFFERENTIATION FACTOR 16 PRECURSOR PROTEIN.
 GN GDF16.
 OS Xenopus laevis (African clawed frog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 CC Xenopodinae; Xenopus.
 OX NCBI_TaxID: 8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed 10906478;
 RA Vokes S.A., Kried P.A.;
 RT "Gdf16, a novel member of the growth/differentiation factor subgroup
 RT of the IGF-beta superfamily, is expressed in the hindbrain and
 RT epibranchial placodes."
 RL Mech. Dev. 95:279-282(2000).
 CC -1- SIMILARITY: TO THE IGF-BETA FAMILY.
 DR EMBL: AF239676; AAF99597.1; -.
 DR InterPro: IPR001839; IGF-beta.
 DR InterPro: IPR001111; TGF-beta.
 DR Pfam: PF00019; IGF-beta; 1.
 DR Pfam: PF00688; IGF_beta_propeptide; 1.
 DR ProDom: PD000457; IGF-beta; 1.
 DR SMART: SM00204; IGF-beta; 1.
 DR PROSITE: PS00250; TGF_BETA; 1.
 KW Glycoprotein; Signal 23. POTENTIAL.
 FT SIGNAL 1
 SQ SEQUENCE 413 AA: 46510 MW: 5F16D7D97E591F6 CR664;

Query Match 81.2%; Score 527; DB 13; Length 413;
 Best Local Similarity 77.4%; Pred. No. 4,90-52;
 Matches 92; Conservative 13; Mismatches 14; Indels 0; Gaps 0;
 QY 1 PLATRUCKRPSKNIKARSRKALHNPKDMGWIMLAPLEYEAFHCEGLCEPFLRSKLE 60
 DB 295 PTINNGKGHAKKSKTRCKSKKPLLVNFKELGWIMLAPLEYEAFHCEGLCEPFLRSKLE 454
 QY 61 PTNHAVIQTILMNSMDPESTPTACVPTKLSPTLSILFSDSANNVVKYQYEMVVESSGR 119
 DB 455 PTNHAIQTILMNSMDPESTPTSCCVSKLSPTLSILFSDSANNVVKYQYEMVVESSGR 413

RESULT 7
 QW754
 ID QW754 PRELIMINARY: PRI: 499 AA.
 AC QW754
 DT 01-NOV-1999 (FEMBLrel. 12, Created)
 DT 01-NOV-1999 (FEMBLrel. 12, Last sequence update)
 DT 01-JUN-2001 (FEMBLrel. 17, Last annotation update)
 DE GROWTH AND DIFFERENTIATION FACTOR 6.
 GN GDF6.
 OS Xenopus laevis (African clawed frog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 CC Xenopodinae; Xenopus.
 OX NCBI_TaxID: 8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Chang C., Brumati-Brianou A.;
 RT "Xenopus Gdf6, a new antagonist of noggin and a partner of BMPs."
 RL Development 126:1125-1132(1999).
 CC -1- SIMILARITY: TO THE IGF-BETA FAMILY.
 DR EMBL: AF155125; AAD38402.1; -.
 DR HSSP: P12643; 4RMP.

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0M protein - protein search, using sw model

Run on: March 26, 2002, 06:09:27 : Search time 11.67 seconds
(without alignments)
373,874 Million cell updates/sec

Title: US-09-701-121-2

Perfect score: 649

Sequence: 1 PLATROGKKSNNIKARCSR.....ANNVYKOVDMVVEVSQCR 119

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 46664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_49:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	640	98.6	495	1 GDF5_MOUSE	P43027 mus musculus
2	639	98.5	501	1 GDF5_HUMAN	P43026 homo sapien
3	543	84.7	125	1 GDF6_MOUSE	P43028 mus musculus
4	528	81.4	436	1 GDF6_BOVIN	P55106 bos taurus
5	493	76.0	151	1 GDF7_MOUSE	P43029 mus musculus
6	453.5	54.5	461	1 DVRL_STRPO	P48969 strongyloce
7	452	54.2	395	1 UNIV_STRPO	P48970 strongyloce
8	447	53.5	393	1 BMP2_RAT	P49001 rattus norv
9	447	53.5	394	1 BMP2_MOUSE	P21274 mus musculus
10	447	53.5	395	1 BMP2_RABIT	P46564 oryctolagus
11	447	53.5	396	1 BMP2_DAMIA	Q19006 dama dama
12	447	53.5	396	1 BMP2_HUMAN	P12643 homo sapien
13	447	53.5	401	1 BMP4_XENLA	P10885 xenopus lae
14	447	53.5	593	1 DECA_DROSI	P91706 drosophila
15	446	53.3	405	1 BMP4_CHICK	Q90752 gallus gall
16	444	53.0	588	1 DECA_DROME	P07713 drosophila
17	443	52.9	398	1 BMP4_XENLA	P25703 xenopus lae
18	443	52.9	398	1 BMP8_XENLA	P10884 xenopus lae
19	441	52.5	408	1 BMP4_MOUSE	P1275 mus musculus
20	441	52.5	408	1 BMP4_RAT	Q06826 rattus norv
21	439	52.2	408	1 BMP4_HUMAN	P12644 homo sapien
22	438	52.1	372	1 DECA_TRICA	P12644 homo sapien
23	438	52.1	408	1 BMP4_DAMIA	Q29607 dama dama
24	437	51.9	353	1 BMP2_CHICK	Q90751 gallus gall
25	436	51.8	409	1 BMP4_RABIT	Q46576 oryctolagus
26	435	51.6	355	1 DVRL_HHARE	P15621 brachydanio
27	434	51.5	621	1 DECA_DROPS	P91699 drosophila
28	433	51.3	207	1 BMP6_RAT	Q04906 rattus norv
29	433	51.3	452	1 BMP5_MOUSE	P49003 mus musculus
30	433	51.3	454	1 BMP5_HUMAN	P22003 homo sapien
31	432	51.2	513	1 BMP6_HUMAN	P22004 homo sapien
32	430	50.8	431	1 BMP7_HUMAN	P18075 homo sapien
33	429	50.7	510	1 BMP6_MOUSE	P20722 mus musculus

ALIGNMENTS

RESULT 1	ID	GDF5_MOUSE	STANDARD	PR1	495 AA
AC	P43027				
DI	01-NOV-1995	(Rel. 42, Created)			
DI	01-NOV-1995	(Rel. 42, Last sequence update)			
DI	20-AUG-2001	(Rel. 40, Last annotation update)			
DE	GROWTH/DIFFERENTIATION FACTOR 5 PRECURSOR (GDF-5)				
GN	GDF5 OR GDF-5 OR DF				
OS	Mus musculus (Mouse)				
CC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;				
CC	NBT_LuxID: 10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN Cl-1; TISSUE Embryo;				
EX	MEDLINE: 94195427; PubMed: 8145850;				
RA	Storm E.E., Haynh T.V., Copeland N.G., Jenkins N.A., Kinastey D.M.,				
RA	Lee S.-J.;				
R1	*Limb alterations in brachypodism mice due to mutations in a new				
RT	member of the TGF beta-superfamily.";				
RL	Nature 368:639-644(1994).				
CC	-1- FUNCTION: COULD BE INVOLVED IN BONE FORMATION.				
CC	-1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).				
CC	-1- DISEASE: DEFECTS IN GDF-5 ARE THE CAUSE OF BRAHYPODISM WHICH				
CC	ALTERS THE LENGTH AND NUMBERS OF BONES IN THE LIMBS BUT SPARES THE				
CC	AXIAL SKELETON.				
CC	-1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.				
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CC	OR SEND AN EMAIL TO license@isb-sib.ch).				
CC	EMBL: 008347; AAA18778.1; -				
DR	ISSP; P18075; 1IMP.				
DR	MGU; MG1:95688; Gdf5.				
DR	InterPro: IPR002400; GFCysKnot.				
DR	InterPro: IPR001849; TGF-beta.				
DR	InterPro: IPR001111; TGF-beta.				
DR	PIam; PF00019; TGF beta; 1.				
DR	PIam; PF000688; TGF-beta-propeptide; 1.				
DR	PKINIS; P000438; GFCYSKNOT.				
DR	ProDom; P000457; TGF-beta; 1.				
DR	SMART; SM0204; IGFB; 1.				
DR	PROSITE; PS00250; TGF-BETA_1; 1.				
KW	SIGNAL; Growth factor; Cytokine; Glycoprotein; Polymorphism.				
FT	SIGNAL	1	27	POTENTIAL.	
FT	PROPEP	28	375	POTENTIAL.	
FT	CHAIN	476	495	GROWTH/DIFFERENTIATION FACTOR 5.	
FT	DISULFID	494	460	BY SIMILARITY.	
FT	DISULFID	423	492	BY SIMILARITY.	
FT	DISULFID	427	494	BY SIMILARITY.	

P10886 xenopus lae
P24359 mus musculus
P44820 homo sapien
P44821 mus musculus
P09534 xenopus lae
P27091 drosophila
Q24735 gallus gall
Q95393 drosophila
Q91229 homo sapien
Q99556 mus musculus
Q99123 homo sapien

44 428 525.5 425 1 BMP7_XENLA
45 427 50.4 430 1 BMP7_MOUSE
46 317.5 48.9 402 1 BMP8_HUMAN
47 314.5 48.5 499 1 BMP8_MOUSE
48 313 48.2 360 1 DVRL_XENLA
49 304 46.8 455 1 G0A_DROME
50 303 46.7 427 1 DSI1_CHICK
51 302 46.5 436 1 G0A_DROVI
52 300.5 46.3 424 1 BMP10_HUMAN
53 297.5 45.8 420 1 BMP10_MOUSE
54 294.5 45.2 428 1 GDF2_MOUSE
55 291.5 44.5 464 1 GDF3_HUMAN

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DR EMBL: U08438; AAA18779.1; 1.
DR RSP: P18075; IEMP.
DR MGI: MGI:95689; Gdf6.
DR InterPro: IPR001839; TGF-beta.
DR Pfam: PF00019; TGF-beta; 1.
DR Problem: P0000357; TGF-beta; 1.
DR SMART: SM00204; TGF-beta; 1.
DR PROSITE: PS00250; TGF-beta; 1.
KW Growth factor; cytokine; glycoprotein.
FT N-TER 1 1
FT PROPEP 31 5. POTENTIAL.
FT CHAIN 6 125 GROWTH/DIFFERENTIATION FACTOR 6.
FT DISULFID 24 90 BY SIMILARITY.
FT DISULFID 54 122 BY SIMILARITY.
FT DISULFID 57 124 BY SIMILARITY.
FT DISULFID 89 89 INTERCHAIN (BY SIMILARITY).
SQ SEQUENCE 125 AA: 14373 MW: 10FAZA5B748DA42 CRC64;

Query Match 83.78; Score 54.3; DB 1; Length 125;
Best Local Similarity 80.38; Pred. No. 1,26-51;
Matches 94; Conservative 14; Mismatches 10; Indels 0; Gaps 0;

QY 3 ATGCGKRSKSLKARCSKALHVNFKMGWDWMIAPLEYEAFHCEGLAEPFLKSHLEPT 62
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
DB 9 ASKRGKRGKSKSLKARCSKALHVNFKMGWDWMIAPLEYEAFHCEGLAEPFLKSHLEPT 68
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

QY 63 NHAVQTILMNSMDPESTPTACVPTKLSPISTILETUSANNVYKQYEMMVESGGR 119
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
DB 69 NHAVQTILMNSMDPESTPTACVPTKLSPISTILETUSANNVYKQYEMMVESGGR 125
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

RESULT 4
GDF6_BOVIN
ID GDF6_BOVIN STANDARD; PRT; 436 AA.
AC P55106;
DT 01-OCT-1996 (rel. 44, Last sequence update)
DT 20-AUG-2001 (rel. 40, Last annotation update)
DE GROWTH/DIFFERENTIATION FACTOR 6 PRECURSOR (GDF-6) (CARTILAGE-DERIVED
DE MORPHOGENETIC PROTEIN 2) (GDF-2) (FRAGMENT).
GN GDF6 OR GDF2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID 9913;
RN 111
RP SEQUENCE FROM N.A.
RC TISSUE: Articular cartilage;
RX MEDLINE 95050604; PubMed 7961761;
RA Chana S., Hwang R., Thomas J.F., Vukicevic S., Luyten F.P.,
RA Ryba N.J.P., Kozak C.A., Reddi A.H., Mares M.;
RI "Cartilage-derived morphogenetic proteins. New members of the
RI transforming growth factor-beta superfamily predominantly expressed
RI in long bones during human embryonic development.";
RL J. Biol. Chem. 269:28227-28234 (1994).
CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
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DR EMBL: U14661; AAA61416.1; 1.

DR InterPro: IPR001839; TGF-beta.

DR InterPro: IPR00111; TGF-beta.

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DR Pfam: PF00019; TGF-beta; 1.
DR Problem: P0000357; TGF-beta; 1.
DR SMART: SM00204; TGF-beta; 1.
DR PROSITE: PS00250; TGF-beta; 1.
KW Growth factor; cytokine; glycoprotein.
FT N-TER 1 1
FT PROPEP 31 316 POTENTIAL.
FT CHAIN 413 436 GROWTH/DIFFERENTIATION FACTOR 6.
FT DISULFID 445 401 BY SIMILARITY.
FT DISULFID 468 433 BY SIMILARITY.
FT DISULFID 468 445 BY SIMILARITY.
FT DISULFID 400 400 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 27 27 N-LINKED (GLCNAC...?) (POTENTIAL).
FT CARBOHYD 89 89 N-LINKED (GLCNAC...?) (POTENTIAL).
SQ SEQUENCE 436 AA: 47874 MW: 4068B12EFA951D CRC64;

Query Match 81.48; Score 528; DB 1; Length 436;
Best Local Similarity 76.98; Pred. No. 2,10-49;
Matches 90; Conservative 16; Mismatches 11; Indels 0; Gaps 0;

QY 3 ATGCGKRSKSLKARCSKALHVNFKMGWDWMIAPLEYEAFHCEGLAEPFLKSHLEPT 62
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
DB 320 ASHGGKRGKSKSLKARCSKALHVNFKMGWDWMIAPLEYEAFHCEGLAEPFLKSHLEPT 479
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

QY 63 NHAVQTILMNSMDPESTPTACVPTKLSPISTILETUSANNVYKQYEMMVESGGR 119
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
DB 380 NHAVQTILMNSMDPESTPTACVPTKLSPISTILETUSANNVYKQYEMMVESGGR 446
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

RESULT 5
GDF7_MOUSE
ID GDF7_MOUSE STANDARD; PRT; 151 AA.
AC P43029;
DT 01-NOV-1995 (rel. 32, Created)
DT 01-NOV-1995 (rel. 32, Last sequence update)
DT 20-AUG-2001 (rel. 40, Last annotation update)
DE GROWTH/DIFFERENTIATION FACTOR 7 PRECURSOR (GDF-7) (FRAGMENT).
GN GDF7 OR GDF-7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID 10090;
RN 111
RP SEQUENCE FROM N.A.
RC STRAIN BALB/c; TISSUE: Liver;
RX MEDLINE 94195427; PubMed 8145860;
RA Storm E.E., Boych T.V., Copeland N.G., Jenkins N.A., Kingsley D.M.,
RA Leo S.J.;
RI "Limb alterations in brachypodism mice due to mutations in a new
RI member of the TGF-beta superfamily.";
RL Nature 368:69-74 (1994).
CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
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DR EMBL: U08439; AAA18780.1; 1.

DR RSP: P18075; IEMP.

DR MGI: MGI:95690; Gdf7.

DR InterPro: IPR001839; TGF-beta.

DR Pfam: PF00019; TGF-beta; 1.

DR Problem: P0000357; TGF-beta; 1.

DR SMART: SM00204; TGF-beta; 1.

DR PROSITE: PS00250; TGF-beta; 1.

DR HSDP: P18075; HMP.
 DR M3D: M3138177; HMP2.
 DR InterPro: IPR001849; TGF_beta.
 DR InterPro: IPR001111; TGFb_N.
 DR Pfam: PF00019; TGF_beta; 1.
 DR Pfam: PF00698; TGF_beta; 1.
 DR Pfam: PF00698; TGF_beta; 1.
 DR ProDom: P000457; TGF_beta; 1.
 DR SMART: SM00204; TGF_beta; 1.
 DR ProSITE: PS00250; TGF_BETA 1; 1.
 KW Signal: Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
 FT SIGNAL: 1 19 POTENTIAL.
 FT PROPEP: 20 280
 FT CHAIN: 281 494 BONE MORPHOGENETIC PROTEIN 2.
 FT DISULFID: 294 359 BY SIMILARITY.
 FT DISULFID: 324 391 BY SIMILARITY.
 FT DISULFID: 427 494 BY SIMILARITY.
 FT DISULFID: 458 458 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD: 134 134 N-LINKED (GLNAC...) (POTENTIAL).
 FT CARBOHYD: 162 162 N-LINKED (GLNAC...) (POTENTIAL).
 FT CARBOHYD: 198 198 N-LINKED (GLNAC...) (POTENTIAL).
 FT CARBOHYD: 336 336 N-LINKED (GLNAC...) (POTENTIAL).
 FT CONFLICT: 110 110 T...S (IN REF. 2).
 FT CONFLICT: 114 114 QL...HE (IN REF. 2).
 FT CONFLICT: 271 271 G...R (IN REF. 2).
 SQ SEQUENCE: 494 AA; 44514 MW; ED6A0F105B7EEF54 CR6944;
 Query Match: 54.5%; Score 347; ID 1; Length 494;
 Best Local Similarity: 54.5%; Prod. No. 5,50 40;
 Matches: 64; Conservative: 17; Mismatches: 44; Indels: 2; Gaps: 2;
 QY 5 RQK RPSKRLKARSKKALIVNFKDMDWDTAPLEYAFRTEHCTEFLSHLEIN 63
 DB 280 RQK RPSKRLKARSKKALIVNFKDMDWDTAPLEYAFRTEHCTEFLSHLEIN 63
 QY 64 HAVTQTLNMSMDPSTPTACVPTPLSPISLPLFUSANNVYKQFLMVVSGGR 119
 DB 440 HAVTQTLNMSVSN SKIPKACGVPTLSATLSMLYDENEKVLYKNYQDMVVVSGGR 494
 RESULT 10
 HMP2_RAUIT
 ID HMP2_KABIT STANDARD; PRT: 495 AA.
 AC 045664;
 DT 15 JUL 1999 (Ref. 48, Created)
 DT 15 JUL 1999 (Ref. 48, Last sequence update)
 DT 20 AUG 2001 (Ref. 40, Last annotation update)
 DE BONE MORPHOGENETIC PROTEIN 2 PRECURSOR (HMP 2).
 GN HMP2 OR HMP-2.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 CX NCBI TaxID 9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN NEW ZEALAND WHITE; TISSUE: ocular ciliary epithelium;
 RA Wan X.L., Sears J., Chen S., Sears M.;
 RI "Cloning and expression of HMP-2/-4 from rabbit ocular ciliary
 epithelium."
 RT Submitted (JAN 1998) to the EMBL/GenBank/DBS databases.
 RL
 CC 1- FUNCTION: INDUCES CAPITAGE AND BONE FORMATION (BY SIMILARITY).
 CC 1- SUBUNIT: HOMODIMER; DISULFIDE LINKED (BY SIMILARITY).
 CC 1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 CC
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 CC or send an email to license@isb.sib.ch).
 CC
 DB EMBL: AF041421; AA096785.1;

DR InterPro: IPR002405; Intubulin_alpha.
 DR InterPro: IPR001849; TGF_beta.
 DR InterPro: IPR001111; TGFb_N.
 DR Pfam: PF00019; TGF_beta; 1.
 DR Pfam: PF00698; TGF_beta; 1.
 DR ProDom: P000457; TGF_beta; 1.
 DR SMART: SM00204; TGF_beta; 1.
 DR ProSITE: PS00250; TGF_BETA 1; 1.
 KW Signal: Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
 FT SIGNAL: 1 23 POTENTIAL.
 FT PROPEP: 24 281
 FT CHAIN: 282 495 BONE MORPHOGENETIC PROTEIN 2.
 FT DISULFID: 295 360 BY SIMILARITY.
 FT DISULFID: 324 392 BY SIMILARITY.
 FT DISULFID: 428 494 BY SIMILARITY.
 FT DISULFID: 459 459 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD: 134 134 N-LINKED (GLNAC...) (POTENTIAL).
 FT CARBOHYD: 199 199 N-LINKED (GLNAC...) (POTENTIAL).
 FT CARBOHYD: 337 337 N-LINKED (GLNAC...) (POTENTIAL).
 SQ SEQUENCE: 495 AA; 44664 MW; B01DCCYD6W58456 CR6944;
 Query Match: 54.5%; Score 347; ID 1; Length 495;
 Best Local Similarity: 54.5%; Prod. No. 5,50 40;
 Matches: 64; Conservative: 17; Mismatches: 44; Indels: 2; Gaps: 2;
 QY 5 RQK RPSKRLKARSKKALIVNFKDMDWDTAPLEYAFRTEHCTEFLSHLEIN 63
 DB 280 RQK RPSKRLKARSKKALIVNFKDMDWDTAPLEYAFRTEHCTEFLSHLEIN 63
 QY 64 HAVTQTLNMSMDPSTPTACVPTPLSPISLPLFUSANNVYKQFLMVVSGGR 119
 DB 440 HAVTQTLNMSVSN SKIPKACGVPTLSATLSMLYDENEKVLYKNYQDMVVVSGGR 495
 RESULT 11
 HMP2_DAMIA
 ID HMP2_DAMIA STANDARD; PRT: 496 AA.
 AC 019006;
 DT 15 JUL 1998 (Ref. 46, Created)
 DT 15 JUL 1998 (Ref. 46, Last sequence update)
 DT 20 AUG 2001 (Ref. 40, Last annotation update)
 DE BONE MORPHOGENETIC PROTEIN 2 PRECURSOR (HMP 2).
 GN HMP2.
 OS Lama lama (Fallow deer) (Capreolus dama).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae.
 CX NCBI TaxID 40542;
 RN [1]
 RP SEQUENCE FROM N.A.
 RT TISSUE: Adipose.
 RX MEDLINE 97157076; PubMed 9004457;
 RA Ford J.Q., Chen D., Ghosh Choudhury N., Esparza J., Mundy G.R.,
 RA Harris S.E.;
 RI "Bone morphogenetic protein 2 transcripts in rapidly developing deer
 antler tissue contain an extended 5' non coding region arising from a
 distal promoter."
 RT Submitted (JAN 1997) to the EMBL/GenBank/DBS databases.
 RL
 CC 1- FUNCTION: INDUCES CAPITAGE AND BONE FORMATION.
 CC 1- SUBUNIT: HOMODIMER; DISULFIDE LINKED.
 CC 1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 CC
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 CC
 DB EMBL: AJ001817; CA000444.1;


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DB 477 RFRPPTKKNHDTTCRHSISLYVPSDWGWDWVAPIGYDAYYCHGKCPPEPLADHFNST 536
QY 63 NHAVIQILMNSMDPESTPTTACVPTLSPISILFIDSANNVVYKQYELMVVSGGCR 119
DB 537 NHAVQVILVNNMNPQKVPKACVPTQLDLSVAMLYLNVUSTVLKANYOHMIVVGGCR 594

RESULT 15
BMP4_CHICK
ID BMP4_CHICK STANDARD; PRT: 405 AA.
AC Q90752;
DI 01-NOV-1997 (rel. 35, Created)
DI 01-NOV-1997 (rel. 35, Last sequence update)
DI 20-AUG-2001 (rel. 40, Last annotation update)
DE BONE MORPHOGENETIC PROTEIN 4 PRECURSOR (BMP-4).
GN BMP4 OR BMP-4.
OS Gallus gallus (chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neornithae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID 9031;
RN 11;
RP SEQUENCE FROM N.A.
RC STRAIN WHITE LEGHORN;
RA MEDLINE 94161974; PubMed 1119128;
RA Francis P.H., Richardson M.K., Brickell P.M., Pickle C.;
RI "Bone morphogenetic proteins and a signalling pathway that controls
RI patterning in the developing chick limb.";
RI Development 120:209-218(1994).
RN 12;
RP FUNCTION.
RX PubMed 9927590;
RA Pizette S., Niswander L.;
RI "BMPs negatively regulate structure and function of the limb apical
RI ectodermal ridge.";
RL Development 126:883-894(1999).
CC -1- FUNCTION: NEGATIVELY REGULATES THE STRUCTURE AND FUNCTION OF THE
CC LIMB APICAL ECTODERMAL RIDGE.
CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC -----
DR EMBL: X75915; CAA53514.1; -.
DR HSSP: P18075; BMP.
DR InterPro: IPR001839; TGF-beta.
DR InterPro: IPR001111; TGFb_N.
DR Pfam: PF00019; tgf-beta; 1.
DR Pfam: PF00688; tgf-beta; 1.
DR ProDom: PD000457; TGF-beta; 1.
DR SMART: SM00204; TGF-beta; 1.
DR PROSITE: PS00250; TGF-BETA_1; 1.
KW Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
FT SIGNAL 1 19 POTENTIAL.
FT PROPEP 20 291 BY SIMILARITY.
FT CHAIN 292 405 BONE MORPHOGENETIC PROTEIN 4.
FT DISULFID 405 470 BY SIMILARITY.
FT DISULFID 444 402 BY SIMILARITY.
FT DISULFID 448 404 BY SIMILARITY.
FT DISULFID 469 369 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 144 144 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 208 208 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 347 347 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 362 362 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 405 AA; 4605 MW; 544302DBA0A0F81C9C64;

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Query Match 53.8% Score 546; DB 1; Length 405;
Best Local Similarity 52.1% Prod. No. 7.4e-40;
Matches 64; Conservative 21; Mismatches 41; Indels 6; Gaps 2;
QY 4 TRCKRP...SKNLRKCRSKAHVNFKMGWIDWIAPLEYEAHCHGLTEFPLRSH 98
DB 286 TRKRRSPKHGSRKKNKKNCRHLYVDFSLVGVNWDWIVAPGYQAYCHGKCPPEPLADH 445
QY 59 LEPINHAVIQILMNSMDPESTPTTACVPTLSPISILFIDSANNVVYKQYELMVVSGGCR 118
DB 446 LNSTNHAVIQILVNSVN-SSUPKACVPTELSLSMLYLDLYIKVLIKNTQEMVVEGGC 404
QY 119 R 119
DB 405 R 405

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Job time: 197 sec

